

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: August 5, 2005, 19:13:20 ; Search time 172 Seconds
(without alignments)
1054.597 Million cell updates/sec

Title: US-10-063-565-58
Sequence: 2423
1 MLCCLYVPVIGSAQTEFOY.....VSISVYVENKLTILGVQSR 469
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
2105692 sege, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY66718	standard;	protein;	469	AA.	
DE	Membrane-bound protein				PRO1106.	
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 3;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 2						
ID	AAB87554	standard;	protein;	469	AA.	
DE	Human PRO1106.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 4;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 3						
ID	AAB65241	standard;	protein;	469	AA.	
DE	Human PRO1106 (UNQ549)					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 4;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 4						
ID	ABG95879	standard;	protein;	469	AA.	
DE	Human secreted/transmembrane protein				PRO1106.	
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 5;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 5						
ID	ABU58056	standard;	protein;	469	AA.	
DE	Human PRO polypeptide #88.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 6						
ID	ABU59134	standard;	protein;	469	AA.	
DE	Novel human secreted or transmembrane protein				PRO1106.	

PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 7						
ID	ABU82646	standard;	protein;	469	AA.	
DE	Human secreted/transmembrane protein				PRO1106.	
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 8						
ID	ABU60565	standard;	protein;	469	AA.	
DE	Human secreted/transmembrane protein, #118.					
PN	US2002160384-A1.					
PD	31-OCT-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 9						
ID	ABU13947	standard;	protein;	469	AA.	
DE	Human PRO1106 polypeptide.					
PN	US2002103125-A1.					
PD	01-AUG-2002.					
PA	(GETH) GENENTECH LTD.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 10						
ID	ABU72532	standard;	protein;	469	AA.	
DE	Novel human secreted and transmembrane protein				PRO1106.	
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 11						
ID	ABU90904	standard;	protein;	469	AA.	
DE	Novel human secreted and transmembrane protein				PRO1106.	
PN	US2003018173-A1.					
PD	23-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 12						
ID	ABO33963	standard;	protein;	469	AA.	
DE	Human secreted/transmembrane protein				PRO1106.	
PN	US2003009013-A1.					
PD	09-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 13						
ID	ABU71980	standard;	protein;	469	AA.	
DE	Novel human secreted and transmembrane protein				PRO1106.	
PN	US2003018183-A1.					
PD	23-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 14						
ID	ABU71534	standard;	protein;	469	AA.	
DE	Human secreted polypeptide				PRO1106.	
PN	US2003013855-A1.					
PD	16-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 2423;	DB 6;	Length 469;	
Best Local Similarity		100.0%;	Pred. No. 3e-220;			
RESULT 15						
ID	ABU72315	standard;	protein;	469	AA.	
DE	Human PRO polypeptide #29.					
PN	US2002182638-A1.					
PD	05-DEC-2002.					

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 16
ID ABU90988 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 17
ID ABU59281 standard; protein; 469 AA.
DE Human secreted/transmembrane protein, #118.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 18
ID ABO25978 standard; protein; 469 AA.
DE Human PRO1106 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 19
ID ABO27309 standard; protein; 469 AA.
DE Human secreted/transmembrane polypeptide PRO1106.
PN US200309012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 20
ID ABU92504 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 21
ID ABU81174 standard; protein; 469 AA.
DE Human secreted polypeptide PRO1106.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 22
ID ABO53289 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 23
ID ABU58987 standard; protein; 469 AA.
DE Human secreted/transmembrane protein, #118.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 24
ID ABU92365 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;

RESULT 25
ID ABU59430 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1291.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 26
ID ABU98291 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 27
ID ABU89296 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 28
ID ABU82503 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 29
ID ABU92196 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 30
ID ABU96467 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 31
ID ABU10902 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 32
ID ABU81654 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 33
ID ABU72137 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 34
ID ABU88593 standard; protein; 469 AA.
DE Human secreted and transmembrane polypeptide PRO1106.

PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 35
ID ABO34107 standard; protein; 469 AA.
DE Human PRO1106 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 36
ID ADB17115 standard; protein; 469 AA.
DE Human transmembrane PRO polypeptide (SegID 58).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 37
ID ADA37800 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 38
ID ADA21486 standard; protein; 469 AA.
DE Human secreted/transmembrane polypeptide PRO1106.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 39
ID ABO44267 standard; protein; 469 AA.
DE Human secreted/transmembrane polypeptide PRO 11106.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 40
ID ADA10273 standard; protein; 469 AA.
DE Human secreted/transmembrane protein, PRO1106.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 41
ID ADA19920 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 42
ID ADB17303 standard; protein; 469 AA.
DE Human transmembrane PRO polypeptide (SegID 58).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 43
ID ADA17817 standard; protein; 469 AA.
DE Human PRO1106 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;

RESULT 44
ID ADA27925 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 45
ID ADA20092 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 46
ID ABO34195 standard; protein; 469 AA.
DE Human secreted/transmembrane polypeptide PRO 11106.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 47
ID ADA94505 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 48
ID ADA38730 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 49
ID ADA92851 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 50
ID ADA00389 standard; protein; 469 AA.
DE Human secreted/transmembrane polypeptide PRO 1106.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 51
ID ABO53193 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 52
ID ADA22412 standard; protein; 469 AA.
DE Human secreted/transmembrane polypeptide PRO1106.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 53
ID ABO22563 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003011982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;

RESULT 54
ID ADA06578 standard; protein; 469 AA.
DE Human secreted/transmembrane PRO polypeptide #88.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 55
ID ADA39271 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003058782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 56
ID ADB85631 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 57
ID ADB96297 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 58
ID ADB68310 standard; protein; 469 AA.
DE Human PRO1106 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 59
ID ADB68117 standard; protein; 469 AA.
DE Human PRO1106 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 60
ID ADB90934 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 61
ID ADC57769 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 62
ID ADC55133 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 63
ID ADC12000 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;

Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 64
ID ADC07014 standard; protein; 469 AA.
DE Human PRO1106 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 65
ID ADC56422 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 66
ID ADC17193 standard; protein; 469 AA.
DE Mammalian PRO polypeptide (Seqid 58).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 67
ID ADC07477 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 68
ID ADC11467 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 69
ID ADC14891 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 70
ID ADC52386 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 71
ID ADC14589 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 72
ID ADD08121 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 73
ID ADC81946 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003083461-A1.
PD 01-MAY-2003.


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Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 74
ID ADD07588 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 75
ID ADC82479 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 76
ID ADD08659 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 77
ID ADD06908 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 78
ID ADC83155 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 79
ID ADD55262 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 80
ID ADD36062 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 81
ID ADD56220 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 82
ID ADD54658 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 83
ID ADE26812 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003087304-A1.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 84
ID ADE26279 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 85
ID ADF67216 standard; protein; 469 AA.
DE Human PRO1106 amino acid sequence SEQ ID NO:289.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 86
ID ADC01063 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 87
ID ADG08616 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 88
ID ADF5237 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 89
ID ADH24090 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 90
ID ADH34116 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 91
ID ADH29949 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 92
ID ADH23920 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2423; DB 7; Length 469;
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Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 93
ID ADH85324 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 94
ID ADH24600 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 95
ID ADH37456 standard; protein; 469 AA.
DE Human secreted and transmembrane protein PRO1106.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 96
ID ADH02045 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 97
ID ADH37626 standard; protein; 469 AA.
DE Human secreted and transmembrane protein PRO1106.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 98
ID ADH85664 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 99
ID ADH24260 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 100
ID ADH38554 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 101
ID ADH83675 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;

RESULT 102
ID ADH29483 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 103
ID ADH27599 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 104
ID ADH37796 standard; protein; 469 AA.
DE Human secreted and transmembrane protein PRO1106.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 105
ID ADH37973 standard; protein; 469 AA.
DE Human secreted and transmembrane protein PRO1106.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 106
ID ADH57393 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 107
ID ADH53535 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 108
ID ADH53705 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 109
ID ADH52041 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 110
ID ADH49896 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 111

ID AD125406 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 112
ID ADH90199 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 113
ID AD125576 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 114
ID ADH97750 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 115
ID AD135470 standard; protein; 469 AA.
DE Human PRO polypeptide #88.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 116
ID AD103598 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 117
ID AD11955 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 118
ID ADH90029 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 119
ID ADH99662 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 120
ID ADH98430 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181707-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 121
ID AD11105 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 122
ID AD11615 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 123
ID ADH98260 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 124
ID ADH98600 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 125
ID ADH98090 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 126
ID AD105078 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 127
ID AD103428 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 128
ID AD104823 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 129
ID ADH78277 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181668-A1.
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 130
ID ADI19621 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 131
ID ADH90369 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 132
ID ADI03088 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 133
ID ADH77937 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 134
ID ADH97920 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 135
ID ADI01305 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 136
ID ADI02000 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 137
ID ADI01358 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 138
ID ADI11445 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 139
ID ADI02347 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 140
ID ADI11785 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 141
ID ADI05422 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 142
ID ADH79494 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 143
ID ADI19451 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 144
ID ADI05252 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 145
ID ADH79664 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 146
ID ADI01490 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 147
ID ADI01660 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 148
ID ADI01660 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 7; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
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Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 148
ID AD101830 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 149
ID ADH79834 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 150
ID AD104652 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 151
ID AD102788 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 152
ID ADH78107 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 153
ID AD125746 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 154
ID AD125916 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 155
ID ADK65428 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 156
ID ADH98770 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;

RESULT 157
ID ADH80011 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 158
ID ADJ3742 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 159
ID ADC52196 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003130483-A1.
PD 10-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 160
ID ADP35415 standard; protein; 469 AA.
DE Human PRO1106 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 161
ID ADG11665 standard; protein; 469 AA.
DE Human PRO1106 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 162
ID ADH06628 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 163
ID ADH06458 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 164
ID ADG68879 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 165
ID ADH27769 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 166
ID ADH25110 standard; protein; 469 AA.

DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 167
ID ADH33742 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 168
ID ADH02385 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 169
ID ADH07992 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 170
ID ADG6389 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 171
ID ADH39210 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 172
ID ADG83950 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 173
ID ADH19535 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 174
ID ADG85494 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 175
ID ADH06288 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.

PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 176
ID ADH30118 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 177
ID ADH24430 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 178
ID ADG69559 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 179
ID ADH07822 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 180
ID ADG85834 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 181
ID ADH39380 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 182
ID ADH33572 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 183
ID ADH33912 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 184
ID ADH01122 standard; protein; 469 AA.
DE Human PRO polypeptide #29.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 185
ID ADG69729 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 186
ID ADH21028 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US200322358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 187
ID ADH02215 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 188
ID ADG69219 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 189
ID ADG86004 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 190
ID ADH24940 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 191
ID ADH3557 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 192
ID ADH20066 standard; protein; 469 AA.
DE Human secreted/transmembrane protein PRO1106.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 193
ID ADH02555 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 194
ID ADG69049 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 195
ID ADH07652 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 196
ID ADG86174 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 197
ID ADH24770 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 198
ID ADH25818 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 199
ID ADH38384 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 200
ID ADH57223 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 201
ID ADH52210 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 202
ID ADH49577 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 203
ID ADH49577 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;

Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 203
ID ADH90539 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 204
ID AD11275 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 205
ID ADH98940 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 206
ID AD102170 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 207
ID ADH90709 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 208
ID ADJ98584 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 209
ID ADJ98754 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 210
ID ADH78913 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 211
ID ADJ99147 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 212
ID ADJ99317 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 213
ID ADJ98935 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 214
ID ADH79083 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 215
ID ADK00943 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 216
ID ADK14464 standard; protein; 469 AA.
DE Novel human secreted and transmembrane protein PRO1106.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 217
ID ADM80913 standard; protein; 469 AA.
DE Human PRO polypeptide #29.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2423; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 3e-220;
RESULT 218
ID AAY76084 standard; protein; 469 AA.
DE Murine ADP/ATP transporter family protein, SEQ ID NO:339.
PN W0955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 97.5%; Score 2362; DB 3; Length 469;
Best Local Similarity 97.2%; Pred. No. 1.8e-214;
RESULT 219
ID AAB56023 standard; protein; 469 AA.
DE Skin cell protein, SEQ ID NO: 339.
PN W020069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 97.5%; Score 2362; DB 4; Length 469;
Best Local Similarity 97.2%; Pred. No. 1.8e-214;
RESULT 220
ID ABB72223 standard; protein; 469 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 339.
PN W0200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 97.5%; Score 2362; DB 5; Length 469;
Best Local Similarity 97.2%; Pred. No. 1.8e-214;
RESULT 221

ID AAB42329 standard; protein; 385 AA.
DE Human ORFX ORF2093 polypeptide sequence SEQ ID NO:4186.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 81.3%; Score 1970; DB 3; Length 385;
Best Local Similarity 99.7%; Pred. No. 1.8e-177;
RESULT 222
ID AAM40072 standard; protein; 366 AA.
DE Human polypeptide SEQ ID NO 3217.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 77.8%; Score 1886; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.5e-169;
RESULT 223
ID AAY75964 standard; protein; 312 AA.
DE Murine skin cell protein, SEQ ID 142.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 65.5%; Score 1588; DB 3; Length 312;
Best Local Similarity 97.8%; Pred. No. 2e-141;
RESULT 224
ID AAB55903 standard; protein; 312 AA.
DE Skin cell protein, SEQ ID NO: 142.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 65.5%; Score 1588; DB 4; Length 312;
Best Local Similarity 97.8%; Pred. No. 2e-141;
RESULT 225
ID ABB72103 standard; protein; 312 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 142.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 65.5%; Score 1588; DB 5; Length 312;
Best Local Similarity 97.8%; Pred. No. 2e-141;
RESULT 226
ID AAE23927 standard; protein; 468 AA.
DE Human transporter and ion channel (TRICH) 26.
PN WO200222684-A2.
PD 21-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 64.1%; Score 1554; DB 5; Length 468;
Best Local Similarity 70.6%; Pred. No. 6.3e-138;
RESULT 227
ID AAU27697 standard; protein; 471 AA.
DE Human full-length polypeptide sequence #22.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 64.1%; Score 1554; DB 4; Length 471;
Best Local Similarity 70.6%; Pred. No. 6.3e-138;
RESULT 228
ID ADH42321 standard; protein; 475 AA.
DE Novel human protein NOV56b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 64.1%; Score 1554; DB 8; Length 475;
Best Local Similarity 70.6%; Pred. No. 6.4e-138;
RESULT 229
ID AAU27869 standard; protein; 509 AA.
DE Human conitg polypeptide sequence #22.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 64.1%; Score 1554; DB 4; Length 509;
Best Local Similarity 70.6%; Pred. No. 7.1e-138;
RESULT 230
ID ABJ37928 standard; protein; 468 AA.

DE NOVX protein sequence SEQ ID No 101.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 63.4%; Score 1536; DB 6; Length 468;
Best Local Similarity 69.4%; Pred. No. 3.2e-136;
RESULT 231
ID ADK51034 standard; protein; 468 AA.
DE Human NOV12A protein sequence SeqID54.
PN WO2003083046-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 63.4%; Score 1536; DB 7; Length 468;
Best Local Similarity 69.4%; Pred. No. 3.2e-136;
RESULT 232
ID ADH42319 standard; protein; 468 AA.
DE Novel human protein NOV56a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 63.4%; Score 1536; DB 8; Length 468;
Best Local Similarity 69.4%; Pred. No. 3.2e-136;
RESULT 233
ID AAM79077 standard; protein; 477 AA.
DE Human protein SEQ ID NO 1739.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 61.9%; Score 1501; DB 4; Length 477;
Best Local Similarity 65.8%; Pred. No. 6.8e-133;
RESULT 234
ID AAG71331 standard; protein; 477 AA.
DE Human transporter protein.
PN US2002115136-A1.
PD 22-AUG-2002.
PA (MERK/) MERKULOV G.
PA (YELJ/) YE J.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 61.9%; Score 1501; DB 5; Length 477;
Best Local Similarity 65.8%; Pred. No. 6.8e-133;
RESULT 235
ID ADL15740 standard; protein; 477 AA.
DE Novel human transporter.
PN US2004067523-A1.
PD 08-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 61.9%; Score 1501; DB 8; Length 477;
Best Local Similarity 65.8%; Pred. No. 6.8e-133;
RESULT 236
ID ADC09990 standard; protein; 477 AA.
DE Human NOVX polypeptide SEQ ID NO: 10.
PN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 61.9%; Score 1500; DB 7; Length 477;
Best Local Similarity 65.8%; Pred. No. 8.4e-133;
RESULT 237
ID ADL15742 standard; protein; 475 AA.
DE Rabbit peroxisomal Ca-dependent solute carrier.
PN US2004067523-A1.
PD 08-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 61.7%; Score 1494; DB 8; Length 475;
Best Local Similarity 66.7%; Pred. No. 3.1e-132;
RESULT 238
ID ADA54221 standard; protein; 384 AA.
DE Human protein, SEQ ID 1789.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 60.6%; Score 1469; DB 6; Length 384;
Best Local Similarity 72.1%; Pred. No. 5.3e-130;
RESULT 239
ID ABG22637 standard; protein; 508 AA.
DE Novel human diagnostic protein #22628.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 60.2%; Score 1459; DB 4; Length 508;
Best Local Similarity 66.9%; Pred. No. 7.1e-129;
RESULT 240
ID ABU11651 standard; protein; 467 AA.
DE Human MDDT polypeptide SEQ ID 598.
PN W0200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 55.3%; Score 1340; DB 6; Length 467;
Best Local Similarity 68.6%; Pred. No. 1.2e-117;
RESULT 241
ID ABG30434 standard; protein; 456 AA.
DE Human protein sequence #2 used for determining sequence of unknown gene.
PN JP2002176980-A.
PD 25-JUN-2002.
PA (AISE-) AISIN SEIKI KK.
PA (MEIZ-) MEIZU KK.
Query Match 55.2%; Score 1337.5; DB 5; Length 456;
Best Local Similarity 67.0%; Pred. No. 2e-117;
RESULT 242
ID ADL15743 standard; protein; 410 AA.
DE Human calcium binding transporter #1.
PN US2004067523-A1.
PD 08-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 54.0%; Score 1308; DB 8; Length 410;
Best Local Similarity 66.8%; Pred. No. 1e-114;
RESULT 243
ID ADJ68959 standard; protein; 411 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID765.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 54.0%; Score 1308; DB 7; Length 411;
Best Local Similarity 66.8%; Pred. No. 1e-114;
RESULT 244
ID ABP74120 standard; protein; 480 AA.
DE Human TRICH SEQ ID NO 25.
PN W0200246415-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 52.5%; Score 1273; DB 5; Length 480;
Best Local Similarity 59.8%; Pred. No. 2.7e-111;
RESULT 245
ID AAG65800 standard; protein; 461 AA.
DE Human membrane transporter polypeptide (MTP).
PN W0200174854-A2.
PD 11-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 50.1%; Score 1214.5; DB 4; Length 461;
Best Local Similarity 65.3%; Pred. No. 8.9e-106;
RESULT 246
ID ADL15744 standard; protein; 342 AA.
DE Human calcium binding transporter #2.
PN US2004067523-A1.
PD 08-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 46.3%; Score 1123; DB 8; Length 342;
Best Local Similarity 65.8%; Pred. No. 2.7e-97;
RESULT 247
ID AAB50388 standard; protein; 292 AA.
DE Human uncoupling protein #11.
PN W0200061614-A2.
PD 19-OCT-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 46.2%; Score 1120.5; DB 3; Length 292;
Best Local Similarity 71.3%; Pred. No. 3.6e-97;
RESULT 248
ID ABG30433 standard; protein; 357 AA.
DE Human protein sequence #1 used for determining sequence of unknown gene.
PN JP2002176980-A.
PD 25-JUN-2002.
PA (AISE-) AISIN SEIKI KK.
PA (MEIZ-) MEIZU KK.
Query Match 46.1%; Score 1116; DB 5; Length 357;
Best Local Similarity 68.4%; Pred. No. 1.3e-96;
RESULT 249
ID AAM41858 standard; protein; 226 AA.
DE Human polypeptide SEQ ID NO 6789.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 44.0%; Score 1066.5; DB 4; Length 226;
Best Local Similarity 95.1%; Pred. No. 3.2e-92;
RESULT 250
ID ADN24286 standard; protein; 531 AA.
DE Bacterial polypeptide #6939.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 42.5%; Score 1030.5; DB 8; Length 531;
Best Local Similarity 45.3%; Pred. No. 3e-88;
RESULT 251
ID ABB71306 standard; protein; 370 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40710.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match 39.5%; Score 956; DB 4; Length 370;
Best Local Similarity 54.1%; Pred. No. 2e-81;
RESULT 252
ID AAB47870 standard; protein; 392 AA.
DE Human transporter protein.
PN W0200202635-A2.
PD 10-JAN-2002.
PA (APPL-) APPLERA CORP.
Query Match 38.0%; Score 920; DB 5; Length 392;
Best Local Similarity 49.2%; Pred. No. 5.6e-78;
RESULT 253
ID ADN33117 standard; protein; 345 AA.
DE Human transporter and ion channel (TRICH) protein SeqID2.
PN W02004035755-A2.
PD 29-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 36.1%; Score 874; DB 8; Length 345;
Best Local Similarity 61.2%; Pred. No. 1e-73;
RESULT 254
ID AAB50389 standard; protein; 169 AA.
DE Human uncoupling protein #12.
PN W0200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 35.4%; Score 858; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.2e-72;
RESULT 255
ID AAM53247 standard; protein; 208 AA.
DE Human polypeptide, SEQ ID NO: 2684.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 33.9%; Score 822; DB 4; Length 208;
Best Local Similarity 76.4%; Pred. No. 4.1e-69;
RESULT 256

ID ADL30651 standard; protein: 208 AA.
DE Human protein encoded by a full length cDNA clone seqID 2684.
PN EP136543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 33.9%; Score 822; DB 8; Length 208;
Best Local Similarity 76.4%; Pred. No. 4.1e-69;
RESULT 257
ID AAU87172 standard; protein: 170 AA.
DE Novel central nervous system protein #82.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 33.5%; Score 811; DB 4; Length 170;
Best Local Similarity 97.5%; Pred. No. 3.4e-68;
RESULT 258
ID ADI54487 standard; protein: 170 AA.
DE Novel human protein seq id 690.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 33.5%; Score 811; DB 8; Length 170;
Best Local Similarity 97.5%; Pred. No. 3.4e-68;
RESULT 259
ID ADM05689 standard; protein: 232 AA.
DE Human protein of the invention SEQ ID NO:4574.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 28.0%; Score 679; DB 7; Length 232;
Best Local Similarity 59.4%; Pred. No. 1.7e-55;
RESULT 260
ID AAU87175 standard; protein: 244 AA.
DE Novel central nervous system protein #85.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.9%; Score 579; DB 4; Length 244;
Best Local Similarity 63.0%; Pred. No. 5.5e-46;
RESULT 261
ID ADI54490 standard; protein: 244 AA.
DE Novel human protein seq id 693.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 23.9%; Score 579; DB 8; Length 244;
Best Local Similarity 63.0%; Pred. No. 5.5e-46;
RESULT 262
ID AAM43524 standard; protein: 244 AA.
DE Human polypeptide SEQ ID NO 202.
PN WO200155308-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.7%; Score 575; DB 4; Length 244;
Best Local Similarity 63.0%; Pred. No. 1.3e-45;
RESULT 263
ID AAU19941 standard; protein: 244 AA.
DE Novel human calcium-binding protein #50.
PN WO200155304-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.7%; Score 575; DB 4; Length 244;
Best Local Similarity 63.0%; Pred. No. 1.3e-45;
RESULT 264
ID AAU87490 standard; protein: 244 AA.
DE Novel central nervous system protein #400.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.7%; Score 575; DB 4; Length 244;
Best Local Similarity 63.0%; Pred. No. 1.3e-45;
RESULT 265
ID ADI54805 standard; protein: 244 AA.
DE Novel human protein seq id 1008.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 23.7%; Score 575; DB 8; Length 244;
Best Local Similarity 63.0%; Pred. No. 1.3e-45;
RESULT 266
ID ADM24545 standard; protein: 244 AA.
DE Human PRO polypeptide #28.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.7%; Score 575; DB 8; Length 244;
Best Local Similarity 63.0%; Pred. No. 1.3e-45;
RESULT 267
ID AAM43521 standard; protein: 125 AA.
DE Human polypeptide SEQ ID NO 199.
PN WO200155308-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 566; DB 4; Length 125;
Best Local Similarity 98.2%; Pred. No. 3.4e-45;
RESULT 268
ID AAU19938 standard; protein: 125 AA.
DE Novel human calcium-binding protein #47.
PN WO200155304-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 566; DB 4; Length 125;
Best Local Similarity 98.2%; Pred. No. 3.4e-45;
RESULT 269
ID AAU87487 standard; protein: 125 AA.
DE Novel central nervous system protein #397.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 566; DB 4; Length 125;
Best Local Similarity 98.2%; Pred. No. 3.4e-45;
RESULT 270
ID ADI54802 standard; protein: 125 AA.
DE Novel human protein seq id 1005.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 23.4%; Score 566; DB 8; Length 125;
Best Local Similarity 98.2%; Pred. No. 3.4e-45;
RESULT 271
ID ADM24542 standard; protein: 125 AA.
DE Human PRO polypeptide #25.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 566; DB 8; Length 125;
Best Local Similarity 98.2%; Pred. No. 3.4e-45;
RESULT 272
ID AAB42319 standard; protein: 166 AA.
DE Human ORFX ORF2083 polypeptide sequence SEQ ID NO:4166.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 22.5%; Score 545; DB 3; Length 166;
Best Local Similarity 70.5%; Pred. No. 5.1e-43;
RESULT 273
ID AAG12158 standard; protein: 241 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11160.

PA EPI033405-A2.
ID 06-SEP-2000.
Query Match
Best Local Similarity 22.1%; Score 536; DB 3; Length 241;
PD 06-SEP-2000.

RESULT 274
ID AAG30070 standard; protein; 352 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35884.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 21.4%; Score 519; DB 3; Length 352;
PD 06-SEP-2000.

RESULT 275
ID AAG22634 standard; protein; 138 AA.
DE Novel human diagnostic protein #22625.
PA W0200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 20.6%; Score 500; DB 4; Length 138;
PD 06-SEP-2000.

RESULT 276
ID ADN19851 standard; protein; 438 AA.
DE Bacterial polypeptide #2504.
PA US2003233675-A1.
PD 18-DEC-2003.

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match
Best Local Similarity 19.8%; Score 479; DB 8; Length 438;
PD 06-SEP-2000.

RESULT 277
ID AAG28434 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33649.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 19.1%; Score 462.5; DB 3; Length 330;
PD 06-SEP-2000.

RESULT 278
ID AAG28433 standard; protein; 332 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33648.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 19.1%; Score 462.5; DB 3; Length 332;
PD 06-SEP-2000.

RESULT 279
ID AAG30071 standard; protein; 291 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35885.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 18.7%; Score 452; DB 3; Length 291;
PD 06-SEP-2000.

RESULT 280
ID ABB98661 standard; protein; 332 AA.
DE Amino acid sequence of human transporter and ion channel TRICH-7.
PA W0200296932-A1.
PD 05-DEC-2002.

PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 18.6%; Score 450.5; DB 6; Length 332;
PD 06-SEP-2000.

RESULT 281
ID ABB070830 standard; protein; 139 AA.
DE Human adipocyte Selected Interacting domain, SID, #461.
PA W0200286122-A2.
PD 31-OCT-2002.

PA (HYER-) HYBRIGENICS.
Query Match
Best Local Similarity 18.6%; Score 450; DB 6; Length 139;
PD 06-SEP-2000.

RESULT 282
ID AAY31936 standard; protein; 289 AA.
DE Wheat brittle-1 partial polypeptide.
PA W09949047-A2.
PD 30-SEP-1999.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 17.6%; Score 427.5; DB 2; Length 289;
PD 06-SEP-2000.

RESULT 283
ID AAG29257 standard; protein; 381 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34779.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 17.6%; Score 425.5; DB 3; Length 381;
PD 06-SEP-2000.

RESULT 284
ID AAG29256 standard; protein; 384 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34778.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 17.6%; Score 425.5; DB 3; Length 384;
PD 06-SEP-2000.

RESULT 285
ID AUA44080 standard; protein; 326 AA.
DE Bacterial polypeptide #22510.
PA US2003233675-A1.
PD 18-DEC-2003.

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match
Best Local Similarity 17.5%; Score 423.5; DB 8; Length 326;
PD 06-SEP-2000.

RESULT 286
ID AAG12159 standard; protein; 198 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11161.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 17.3%; Score 420; DB 3; Length 198;
PD 06-SEP-2000.

RESULT 287
ID AAG29005 standard; protein; 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34435.
PA EPI033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 17.1%; Score 415.5; DB 3; Length 415;
PD 06-SEP-2000.

RESULT 288
ID ABB84709 standard; protein; 312 AA.
DE Human diagnostic and therapeutic pproein SEQ ID NO:4958.
PA W02004023973-A2.
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 16.9%; Score 410.5; DB 8; Length 312;
PD 06-SEP-2000.

RESULT 289
ID ABB60506 standard; protein; 377 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8310.
PA W0200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 16.7%; Score 405; DB 4; Length 377;
PD 06-SEP-2000.

RESULT 290
ID ADN20876 standard; protein; 308 AA.
DE Bacterial polypeptide #3529.
PA US2003233675-A1.
PD 18-DEC-2003.

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match
Best Local Similarity 16.0%; Score 386.5; DB 8; Length 308;
PD 06-SEP-2000.

RESULT 291
ID ADN22500 standard; protein; 294 AA.

DE Bacterial polypeptide #5153.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 15.8%; Score 383.5; DB 8; Length 294;
Best Local Similarity 34.8%; Pred. No. 2.4e-27;
RESULT 292
ID AAG49412 standard; protein; 316 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62508.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.8%; Score 383.5; DB 3; Length 316;
Best Local Similarity 30.0%; Pred. No. 2.7e-27;
RESULT 293
ID AAG11516 standard; protein; 316 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10261.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.8%; Score 383.5; DB 3; Length 316;
Best Local Similarity 30.0%; Pred. No. 2.7e-27;
RESULT 294
ID AAG11515 standard; protein; 392 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10260.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.8%; Score 383.5; DB 3; Length 392;
Best Local Similarity 30.0%; Pred. No. 3.7e-27;
RESULT 295
ID AAG49411 standard; protein; 392 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62507.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.8%; Score 383.5; DB 3; Length 392;
Best Local Similarity 30.0%; Pred. No. 3.7e-27;
RESULT 296
ID AAG49410 standard; protein; 411 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62506.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.8%; Score 383.5; DB 3; Length 411;
Best Local Similarity 30.0%; Pred. No. 4e-27;
RESULT 297
ID AAG11514 standard; protein; 411 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10259.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.8%; Score 383.5; DB 3; Length 411;
Best Local Similarity 30.0%; Pred. No. 4e-27;
RESULT 298
ID AAG28435 standard; protein; 266 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33650.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.8%; Score 383; DB 3; Length 266;
Best Local Similarity 33.8%; Pred. No. 2.3e-27;
RESULT 299
ID AAM80061 standard; protein; 182 AA.
DE Human protein SEQ ID NO 3707.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSR-) HYSRQ INC.
Query Match 14.9%; Score 361; DB 4; Length 182;
Best Local Similarity 64.4%; Pred. No. 1.6e-25;
RESULT 300
ID AAG29258 standard; protein; 267 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34780.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 14.7%; Score 355.5; DB 3; Length 267;

Best Local Similarity 30.7%; Pred. No. 9.4e-25;
RESULT 301
ID AAG30072 standard; protein; 226 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35886.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 14.6%; Score 354.5; DB 3; Length 226;
Best Local Similarity 35.1%; Pred. No. 9.1e-25;
RESULT 302
ID ADN19529 standard; protein; 326 AA.
DE Bacterial polypeptide #2182.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.6%; Score 354; DB 8; Length 326;
Best Local Similarity 28.9%; Pred. No. 1.8e-24;
RESULT 303
ID AAG06090 standard; protein; 335 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 2737.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 14.5%; Score 351.5; DB 3; Length 335;
Best Local Similarity 30.1%; Pred. No. 3.4e-24;
RESULT 304
ID ABUS3220 standard; protein; 303 AA.
DE Human metabolism-associated DKFZphes3_35n12 homologue #2.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GERH-) GERMAN HUMAN GENOME PROJECT.
Query Match 14.5%; Score 350.5; DB 4; Length 303;
Best Local Similarity 30.2%; Pred. No. 3.4e-24;
RESULT 305
ID ADG3590 standard; protein; 357 AA.
DE Bacterial polypeptide #22020.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.4%; Score 349; DB 8; Length 357;
Best Local Similarity 27.6%; Pred. No. 6e-24;
RESULT 306
ID AAG29006 standard; protein; 273 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34436.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 14.4%; Score 348.5; DB 3; Length 273;
Best Local Similarity 31.9%; Pred. No. 4.5e-24;
RESULT 307
ID AAG12160 standard; protein; 163 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11162.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 14.2%; Score 343; DB 3; Length 163;
Best Local Similarity 44.0%; Pred. No. 6.9e-24;
RESULT 308
ID ADN20637 standard; protein; 342 AA.
DE Bacterial polypeptide #3290.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.1%; Score 340.5; DB 8; Length 342;
Best Local Similarity 28.1%; Pred. No. 3.6e-23;

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RESULT 309
ID AAG52582 standard; protein; 336 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66859.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.7%; Score 331.5; DB 3; Length 336;
Pred. No. 2.5e-22;
RESULT 310
ID AAG14675 standard; protein; 336 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14628.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.7%; Score 331.5; DB 3; Length 336;
Pred. No. 2.5e-22;
RESULT 311
ID AAG14674 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14627.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.7%; Score 331.5; DB 3; Length 346;
Pred. No. 2.6e-22;
RESULT 312
ID AAG52581 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66858.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.7%; Score 331.5; DB 3; Length 346;
Pred. No. 2.6e-22;
RESULT 313
ID AAG14673 standard; protein; 348 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14626.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.7%; Score 331.5; DB 3; Length 348;
Pred. No. 2.6e-22;
RESULT 314
ID AAG52580 standard; protein; 348 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66857.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.7%; Score 331.5; DB 3; Length 348;
Pred. No. 2.6e-22;
RESULT 315
ID AAB92372 standard; protein; 348 AA.
DE Herbicidially active polypeptide SEQ ID NO: 1583.
PN WC00210210-A2.
PD 07-FEB-2002.
PA (FARR) BAYER AG.
Query Match
Best Local Similarity 13.7%; Score 331.5; DB 5; Length 348;
Pred. No. 2.6e-22;
RESULT 316
ID AAG06857 standard; protein; 333 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3786.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.6%; Score 330.5; DB 3; Length 333;
Pred. No. 3.1e-22;
RESULT 317
ID AAG06856 standard; protein; 350 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3785.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.6%; Score 330.5; DB 3; Length 350;
Pred. No. 3.3e-22;
RESULT 318
ID AAG06855 standard; protein; 368 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3784.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.6%; Score 330.5; DB 3; Length 368;
Pred. No. 3.6e-22;
RESULT 319
ID ADN19721 standard; protein; 322 AA.
DE Bacterial polypeptide #2374.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 13.5%; Score 328; DB 8; Length 322;
Pred. No. 5e-22;
RESULT 320
ID AAB74108 standard; protein; 502 AA.
DE Human TRICH SEQ ID NO: 13.
PN WO200246415-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 13.5%; Score 328; DB 5; Length 502;
Pred. No. 9.8e-22;
RESULT 321
ID ADN20982 standard; protein; 395 AA.
DE Bacterial polypeptide #3635.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 13.5%; Score 327.5; DB 8; Length 395;
Pred. No. 7.6e-22;
RESULT 322
ID AAB82700 standard; protein; 381 AA.
DE A. thaliana acenylate transporter.
PN WO200290506-A2.
PD 14-NOV-2002.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match
Best Local Similarity 13.5%; Score 327; DB 6; Length 381;
Pred. No. 8e-22;
RESULT 323
ID AAG37264 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45792.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 346;
Pred. No. 8.6e-22;
RESULT 324
ID AAG37261 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45788.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 346;
Pred. No. 8.6e-22;
RESULT 325
ID AAG36577 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44845.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 346;
Pred. No. 8.6e-22;
RESULT 326
ID AAG34460 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47451.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 346;
Pred. No. 8.6e-22;
RESULT 327
ID AAG37260 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45787.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 363;
Pred. No. 9.3e-22;
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RESULT 328
ID AAG38459 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47450.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 363;
Pred. No. 9.3e-22;
RESULT 329
ID AAG37263 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45791.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 363;
Pred. No. 9.3e-22;
RESULT 330
ID AAG36576 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44844.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 363;
Pred. No. 9.3e-22;
RESULT 331
ID AAG38458 standard; protein; 381 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47449.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 381;
Pred. No. 1e-21;
RESULT 332
ID AAG36575 standard; protein; 381 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44843.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 381;
Pred. No. 1e-21;
RESULT 333
ID AAG37259 standard; protein; 381 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45786.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 381;
Pred. No. 1e-21;
RESULT 334
ID AAG37262 standard; protein; 381 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45790.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 381;
Pred. No. 1e-21;
RESULT 335
ID AAG38672 standard; protein; 992 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47744.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 992;
Pred. No. 4.2e-21;
RESULT 336
ID AAG36671 standard; protein; 1009 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47743.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 1009;
Pred. No. 4.3e-21;
RESULT 337
ID AAG36670 standard; protein; 1027 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47742.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.5%; Score 326; DB 3; Length 1027;
Pred. No. 4.4e-21;
RESULT 338
ID AAG53541 standard; protein; 810 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68176.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.4%; Score 325; DB 3; Length 810;
Pred. No. 3.5e-21;
RESULT 339
ID AAG53540 standard; protein; 823 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68175.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.4%; Score 325; DB 3; Length 823;
Pred. No. 3.5e-21;
RESULT 340
ID AAG17731 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18863.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.4%; Score 325; DB 3; Length 346;
Pred. No. 1.1e-21;
RESULT 341
ID AAG17730 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18862.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.4%; Score 325; DB 3; Length 363;
Pred. No. 1.2e-21;
RESULT 342
ID AAG17729 standard; protein; 381 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18861.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.4%; Score 325; DB 3; Length 381;
Pred. No. 1.2e-21;
RESULT 343
ID AAM85766 standard; protein; 329 AA.
DE Mouse protein sequence mCPI18836.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 13.4%; Score 324; DB 7; Length 329;
Pred. No. 1.1e-21;
RESULT 344
ID AAB60102 standard; protein; 229 AA.
DE Human transport protein TPPT-22.
PN W0200078953-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 13.4%; Score 324; DB 4; Length 229;
Pred. No. 7.2e-22;
RESULT 345
ID AAB26280 standard; protein; 308 AA.
DE Aspergillus fumigatus essential gene protein #938.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.3%; Score 323; DB 6; Length 308;
Pred. No. 1.4e-21;
RESULT 346
ID AAB25680 standard; protein; 308 AA.
DE Aspergillus fumigatus essential gene protein #338.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 13.3%; Score 323; DB 6; Length 308;
Pred. No. 1.4e-21;
RESULT 347
ID AAM000106 standard; protein; 386 AA.
DE ADP/ATP carrier protein sequence #174.
PN W0200144476-A2.
PD 21-JUN-2001.
PA (BADT) BASF PLANT SCI GMBH.
Query Match
Best Local Similarity 13.3%; Score 323; DB 4; Length 386;
Pred. No. 2e-21;
RESULT 348
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ID ADM19223 standard; protein; 309 AA.
DE Bacterial polypeptide #1876.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.0%; Score 322; DB 8; Length 309;
Best Local Similarity 28.8%; Pred. No. 1.7e-21;
RESULT 349
ID ABB81267 standard; protein; 379 AA.
DE Arabidopsis thaliana protein #95 modulated by PTGS.
PN W0200281695-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH MIESCHER INST.
Query Match 13.2%; Score 321; DB 6; Length 379;
Best Local Similarity 28.9%; Pred. No. 3e-21;
RESULT 350
ID ABB73357 standard; protein; 301 AA.
DE Candida albicans essential protein SEQ ID NO 7194.
PN W0200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.1%; Score 316.5; DB 5; Length 301;
Best Local Similarity 28.7%; Pred. No. 5.6e-21;
RESULT 351
ID ADJ68825 standard; protein; 298 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1631.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.0%; Score 316; DB 7; Length 298;
Best Local Similarity 29.7%; Pred. No. 6.1e-21;
RESULT 352
ID ADA22674 standard; protein; 293 AA.
DE A. gossypii transport protein from Oligo 163 SEQ ID 18.
PN W02003014353-A2.
PD 20-FEB-2003.
PA (BADI) BASF AG.
Query Match 13.0%; Score 315.5; DB 6; Length 293;
Best Local Similarity 30.3%; Pred. No. 6.7e-21;
RESULT 353
ID ABG7659 standard; protein; 322 AA.
DE Fruit fly SODP1 protein.
PN W0200242455-A2.
PD 30-MAY-2002.
PA (DEVE-) DEWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 13.0%; Score 315; DB 5; Length 322;
Best Local Similarity 30.0%; Pred. No. 8.6e-21;
RESULT 354
ID AAG06091 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 2738.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.0%; Score 314.5; DB 3; Length 305;
Best Local Similarity 28.6%; Pred. No. 8.8e-21;
RESULT 355
ID AAY7103 standard; protein; 298 AA.
DE Human adenine nucleotide translocator ANT3.
PN W0200026370-A2.
PD 11-MAY-2000.
PA (MITO-) MITOKOR.
Query Match 13.0%; Score 314; DB 3; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 356
ID AAU01200 standard; protein; 298 AA.
DE Human adenine nucleotide translocator-3 (ANT-3) protein.
PN W0200132876-A2.
PD 10-MAY-2001.

PA (MITO-) MITOKOR.
Query Match 13.0%; Score 314; DB 4; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 357
ID AAM39641 standard; protein; 298 AA.
DE Human polypeptide SEQ ID NO 2786.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 314; DB 4; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 358
ID AAU10380 standard; protein; 298 AA.
DE Human adenine nucleotide translocator 3 (ANT3).
PN W0200185944-A2.
PD 15-NOV-2001.
PA (MITO-) MITOKOR.
Query Match 13.0%; Score 314; DB 5; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 359
ID ADI63017 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 460.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 13.0%; Score 314; DB 7; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 360
ID ADI63016 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 459.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 13.0%; Score 314; DB 7; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 361
ID ADI62996 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 439.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 13.0%; Score 314; DB 7; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 362
ID ADI62744 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 187.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 13.0%; Score 314; DB 7; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 363
ID ADI63018 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 461.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 13.0%; Score 314; DB 7; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 364
ID ADI62998 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 441.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 13.0%; Score 314; DB 7; Length 298;
Best Local Similarity 30.1%; Pred. No. 9.5e-21;
RESULT 365
ID ADI63001 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 444.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.

Query Match	13.0%;	Score 314;	DB 7;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 366				
ID AD163019 standard; protein; 298 AA.				
DE Human apoptosis-associated protein SEQ ID 462.				
PN WO2003058021-A2.				
PD 17-JUL-2003.				
PA (XANT-) XANTOS BIOMEDICINE AG.				
Query Match	13.0%;	Score 314;	DB 7;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 367				
ID AD162984 standard; protein; 298 AA.				
DE Human apoptosis-associated protein SEQ ID 427.				
PN WO2003058021-A2.				
PD 17-JUL-2003.				
PA (XANT-) XANTOS BIOMEDICINE AG.				
Query Match	13.0%;	Score 314;	DB 7;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 368				
ID AD163003 standard; protein; 298 AA.				
DE Human apoptosis-associated protein SEQ ID 446.				
PN WO2003058021-A2.				
PD 17-JUL-2003.				
PA (XANT-) XANTOS BIOMEDICINE AG.				
Query Match	13.0%;	Score 314;	DB 7;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 369				
ID AD163007 standard; protein; 298 AA.				
DE Human apoptosis-associated protein SEQ ID 450.				
PN WO2003058021-A2.				
PD 17-JUL-2003.				
PA (XANT-) XANTOS BIOMEDICINE AG.				
Query Match	13.0%;	Score 314;	DB 7;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 370				
ID AD163009 standard; protein; 298 AA.				
DE Human apoptosis-associated protein SEQ ID 452.				
PN WO2003058021-A2.				
PD 17-JUL-2003.				
PA (XANT-) XANTOS BIOMEDICINE AG.				
Query Match	13.0%;	Score 314;	DB 7;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 371				
ID AD10761 standard; protein; 298 AA.				
DE Human adenine nucleotide translocator ANT3.				
PN US2004146892-A1.				
PD 29-JUL-2004.				
PA (MITO-) MITOKOR INC.				
Query Match	13.0%;	Score 314;	DB 8;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 372				
ID ABW82383 standard; protein; 298 AA.				
DE Tumour-associated antigenic target (TAT) polypeptide PRO83312, SEQ:6120.				
PN WO2004030615-A2.				
PD 15-APR-2004.				
PA (GERTH) GENENTECH INC.				
Query Match	13.0%;	Score 314;	DB 8;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 373				
ID AD189429 standard; protein; 298 AA.				
DE Human adenine nucleotide translocator 3 (ANT3) protein.				
PN US6797467-B1.				
PD 28-SEP-2004.				
PA (MITO-) MITOKOR INC.				
Query Match	13.0%;	Score 314;	DB 8;	Length 298;
Best Local Similarity	30.1%;	Pred. No. 9.5e-21;		
RESULT 374				
ID AAM41427 standard; protein; 323 AA.				
DE Human polypeptide SEQ ID NO 6358.				
PN WO200153312-A1.				
PD 26-JUL-2001.				
PA (HYSE-) HYSEQ INC.				
Query Match	13.0%;	Score 314;	DB 4;	Length 323;

Best Local Similarity	30.1%;	Pred. No. 1.1e-20;
RESULT 375		
ID	ADN23680 standard; protein; 326 AA.	
DE	Bacterial polypeptide #6333.	
PN	US2003233675-A1.	
PD	18-DEC-2003.	
PA	(CAOY/) CAO Y.	
PA	(HINK/) HINKLE G J.	
PA	(SLAT/) SLATER S C.	
PA	(CHEN/) CHEN X.	
PA	(GOLD/) GOLDMAN B S.	
Query Match		
Best Local Similarity	13.0%;	Score 314; DB 8; Length 326;
RESULT 376		
ID	ABBS58702 standard; protein; 360 AA.	
DE	Drosophila melanogaster polypeptide SEQ ID NO 2898.	
PN	WO200171042-A2.	
PD	27-SEP-2001.	
PA	(PEKE) PE CORP NY.	
Query Match		
Best Local Similarity	12.9%;	Score 313; DB 4; Length 360;
RESULT 377		
ID	ADN18797 standard; protein; 307 AA.	
DE	Bacterial polypeptide #1450.	
PN	US2003233675-A1.	
PD	18-DEC-2003.	
PA	(CAOY/) CAO Y.	
PA	(HINK/) HINKLE G J.	
PA	(SLAT/) SLATER S C.	
PA	(CHEN/) CHEN X.	
PA	(GOLD/) GOLDMAN B S.	
Query Match		
Best Local Similarity	12.9%;	Score 312.5; DB 8; Length 307;
RESULT 378		
ID	ADJ70592 standard; protein; 298 AA.	
DE	Human heat mitochondrial protein as a therapeutic target SegID2398.	
PN	WO2003087768-A2.	
PD	23-OCT-2003.	
PA	(MITO-) MITOKOR.	
PA	(BUCK-) BUCK INST AGE RES.	
Query Match		
Best Local Similarity	12.8%;	Score 311; DB 7; Length 298;
RESULT 379		
ID	ADRI0760 standard; protein; 298 AA.	
DE	Human adenine nucleotide translocator ANT2.	
PN	US2004146892-A1.	
PD	29-JUL-2004.	
PA	(MITO-) MITOKOR INC.	
Query Match		
Best Local Similarity	12.8%;	Score 311; DB 8; Length 298;
RESULT 380		
ID	ABJ25994 standard; protein; 395 AA.	
DE	Aspergillus fumigatus essential gene protein #652.	
PN	WO200286090-A2.	
PD	31-OCT-2002.	
PA	(ELIT-) ELITRA PHARM INC.	
Query Match		
Best Local Similarity	12.8%;	Score 310.5; DB 6; Length 395;
RESULT 381		
ID	AAO18516 standard; protein; 298 AA.	
DE	Human insulin receptor signaling modifier SEQ ID NO: 54.	
PN	WO200255664-A2.	
PD	18-JUL-2002.	
PA	(EXEL-) EXELIXIS INC.	
Query Match		
Best Local Similarity	12.8%;	Score 310; DB 5; Length 298;
RESULT 382		
ID	ADJ63038 standard; protein; 298 AA.	
DE	Human apoptosis-associated protein SEQ ID 481.	
PN	WO2003058021-A2.	
PD	17-JUL-2003.	
PA	(XANT-) XANTOS BIOMEDICINE AG.	
Query Match		
Best Local Similarity	12.8%;	Score 310; DB 7; Length 298;

Best Local Similarity 29.4%; Pred. No. 2.3e-20;
RESULT 383
ID ADP54096 standard; protein; 298 AA.
DE Human PRO protein sequence SEQ ID NO:72.
PN W02004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 310; DB 8; Length 298;
Best Local Similarity 29.4%; Pred. No. 2.3e-20;
RESULT 384
ID ADB70048 standard; protein; 310 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3092.
PN W02003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.8%; Score 310; DB 7; Length 310;
Best Local Similarity 28.6%; Pred. No. 2.4e-20;
RESULT 385
ID AAG27856 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32856.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.8%; Score 309.5; DB 3; Length 363;
Best Local Similarity 28.7%; Pred. No. 3.4e-20;
RESULT 386
ID ADN24232 standard; protein; 298 AA.
DE Bacterial polypeptide #6885.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.8%; Score 309; DB 8; Length 298;
Best Local Similarity 28.8%; Pred. No. 2.8e-20;
RESULT 387
ID ADK64910 standard; protein; 318 AA.
DE Disease treating protein complex-derived protein #1561.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZONE AG.
Query Match 12.7%; Score 308.5; DB 7; Length 318;
Best Local Similarity 27.6%; Pred. No. 3.5e-20;
RESULT 388
ID ADN18768 standard; protein; 318 AA.
DE Bacterial polypeptide #1421.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.7%; Score 308.5; DB 8; Length 318;
Best Local Similarity 27.6%; Pred. No. 3.5e-20;
RESULT 389
ID AAM93892 standard; protein; 320 AA.
DE Human polypeptide, SEQ ID NO: 4025.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.7%; Score 308.5; DB 4; Length 320;
Best Local Similarity 27.3%; Pred. No. 3.5e-20;
RESULT 390
ID AAM39031 standard; protein; 320 AA.
DE Human polypeptide SEQ ID NO 2176.
PN W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 308.5; DB 4; Length 320;
Best Local Similarity 27.3%; Pred. No. 3.5e-20;
RESULT 391

ID ADL31992 standard; protein; 320 AA.
DE Human protein encoded by a full length cDNA clone Segid 4025.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY
Query Match 12.7%; Score 308.5; DB 8; Length 320;
Best Local Similarity 27.3%; Pred. No. 3.5e-20;
RESULT 392
ID AAB51794 standard; protein; 329 AA.
DE Gene 21 human secreted protein homologous amino acid sequence #123.
PN W0200061625-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 12.7%; Score 308.5; DB 3; Length 329;
Best Local Similarity 27.8%; Pred. No. 3.6e-20;
RESULT 393
ID ABU53219 standard; protein; 293 AA.
DE Human metabolism-associated DKFZphes3_35n12 homologue #1.
PN W0200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 12.7%; Score 308; DB 4; Length 293;
Best Local Similarity 28.9%; Pred. No. 3.4e-20;
RESULT 394
ID ADO57387 standard; protein; 298 AA.
DE Kidney development associated protein segid 154.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLD/) GOLDING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 12.7%; Score 308; DB 8; Length 298;
Best Local Similarity 29.7%; Pred. No. 3.5e-20;
RESULT 395
ID ABU53218 standard; protein; 315 AA.
DE Human metabolism-associated protein from DKFZphes3_35n12.
PN W0200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 12.7%; Score 307; DB 4; Length 315;
Best Local Similarity 28.6%; Pred. No. 4.7e-20;
RESULT 396
ID AAE21175 standard; protein; 315 AA.
DE Human TRICH-19 protein.
PN W0200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.7%; Score 307; DB 5; Length 315;
Best Local Similarity 28.6%; Pred. No. 4.7e-20;
RESULT 397
ID ADU69924 standard; protein; 315 AA.
DE Human heat mitochondrial protein as a therapeutic target Segid1730.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.7%; Score 307; DB 7; Length 315;
Best Local Similarity 28.6%; Pred. No. 4.7e-20;
RESULT 398
ID AAG43092 standard; protein; 331 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53820.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.7%; Score 307; DB 3; Length 331;
Best Local Similarity 28.3%; Pred. No. 5.1e-20;
RESULT 399
ID AAG14090 standard; protein; 308 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13822.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.6%; Score 305.5; DB 3; Length 308;

Best Local Similarity 30.1%; Pred. No. 6.4e-20;
RESULT 400
ID ADM21564 standard; protein; 368 AA.
DE Bacterial polypeptide #4217.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.6%; Score 305; DB 8; Length 368;
Best Local Similarity 23.4%; Pred. No. 9.3e-20;
RESULT 401
ID ADM18829 standard; protein; 377 AA.
DE Bacterial polypeptide #1482.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.6%; Score 305; DB 8; Length 377;
Best Local Similarity 25.4%; Pred. No. 9.6e-20;
RESULT 402
ID ADI63097 standard; protein; 298 AA.
DE Human apoptosis-associated protein SEQ ID 540.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 12.6%; Score 304.5; DB 7; Length 298;
Best Local Similarity 28.9%; Pred. No. 7.5e-20;
RESULT 403
ID ADJ69874 standard; protein; 298 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1680.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 12.6%; Score 304.5; DB 7; Length 298;
Best Local Similarity 28.9%; Pred. No. 7.5e-20;
RESULT 404
ID AAV71031 standard; protein; 297 AA.
DE Human adenine nucleotide translocator ANTI.
PN WO200026370-A2.
PD 11-MAY-2000.
PA (MITO-) MITOKOR.
Query Match 12.5%; Score 304; DB 3; Length 297;
Best Local Similarity 29.0%; Pred. No. 8.3e-20;
RESULT 405
ID AAU01198 standard; protein; 297 AA.
DE Human adenine nucleotide translocator-1 (ANT-1) protein.
PN WO200132876-A2.
PD 10-MAY-2001.
PA (MITO-) MITOKOR.
Query Match 12.5%; Score 304; DB 4; Length 297;
Best Local Similarity 29.0%; Pred. No. 8.3e-20;
RESULT 406
ID AAU10378 standard; protein; 297 AA.
DE Human adenine nucleotide translocator 1 (ANT1).
PN WO200185844-A2.
PD 15-NOV-2001.
PA (MITO-) MITOKOR.
Query Match 12.5%; Score 304; DB 5; Length 297;
Best Local Similarity 29.0%; Pred. No. 8.3e-20;
RESULT 407
ID ADJ68568 standard; protein; 297 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID374.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.

Query Match 12.5%; Score 304; DB 7; Length 297;
Best Local Similarity 29.0%; Pred. No. 8.3e-20;
RESULT 408
ID ADRI0759 standard; protein; 297 AA.
DE Human adenine nucleotide translocator ANTI.
PN US2004146892-A1.
PD 29-JUL-2004.
PA (MITO-) MITOKOR INC.
Query Match 12.5%; Score 304; DB 8; Length 297;
Best Local Similarity 29.0%; Pred. No. 8.3e-20;
RESULT 409
ID ADR89427 standard; protein; 297 AA.
DE Human adenine nucleotide translocator 1 (ANT1) protein.
PN US6797467-B1.
PD 28-SEP-2004.
PA (MITO-) MITOKOR INC.
Query Match 12.5%; Score 304; DB 8; Length 297;
Best Local Similarity 29.0%; Pred. No. 8.3e-20;
RESULT 410
ID ADS24317 standard; protein; 366 AA.
DE Bacterial polypeptide #13350.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.5%; Score 304; DB 8; Length 366;
Best Local Similarity 24.9%; Pred. No. 1.1e-19;
RESULT 411
ID ADA48102 standard; protein; 382 AA.
DE Rice protein conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.5%; Score 303; DB 6; Length 382;
Best Local Similarity 30.2%; Pred. No. 1.5e-19;
RESULT 412
ID AAB50379 standard; protein; 320 AA.
DE Human uncoupling protein #2.
PN WO200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 302.5; DB 3; Length 320;
Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 413
ID AAM79071 standard; protein; 320 AA.
DE Human protein SEQ ID NO 1733.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 302.5; DB 4; Length 320;
Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 414
ID AAP65101 standard; protein; 320 AA.
DE Hypoxia-induced protein #27.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 12.5%; Score 302.5; DB 5; Length 320;
Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 415
ID ABB62101 standard; protein; 320 AA.
DE Human mitochondrial deoxynucleotide carrier DNC.
PN US2003036111-A1.
PD 20-FEB-2003.
PA (WALK/) WALKER J.
PA (RUNS/) RUNSWICK M.
PA (PALM/) PALMIERI F.
PA (FIER/) FIERMONTI G.
PA (DOLC/) DOLCE V.
Query Match 12.5%; Score 302.5; DB 7; Length 320;

Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 416
ID ADD18694 standard; protein; 320 AA.
DE Human disease related protein Segid125.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 12.5%; Score 302.5; DB 7; Length 320;
Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 417
ID ABM85767 standard; protein; 320 AA.
DE Human protein sequence hCP43032.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 12.5%; Score 302.5; DB 7; Length 320;
Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 418
ID ADL12982 standard; protein; 320 AA.
DE Human steroid-induced C3A liver cell protein #110.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.5%; Score 302.5; DB 8; Length 320;
Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 419
ID ADO58691 standard; protein; 320 AA.
DE Human regulatory molecule HRM-12.
PN US2002058264-A1.
PD 16-MAY-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 12.5%; Score 302.5; DB 8; Length 320;
Best Local Similarity 26.9%; Pred. No. 1.3e-19;
RESULT 420
ID AAM42413 standard; protein; 329 AA.
DE Human polypeptide SEQ ID NO 146.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 302.5; DB 4; Length 329;
Best Local Similarity 26.9%; Pred. No. 1.4e-19;
RESULT 421
ID AAM42411 standard; protein; 329 AA.
DE Human polypeptide SEQ ID NO 144.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 302.5; DB 4; Length 329;
Best Local Similarity 26.9%; Pred. No. 1.4e-19;
RESULT 422
ID ADM20139 standard; protein; 329 AA.
DE Protein encoded by novel human channel/transporter gene #218 clone 2.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 302.5; DB 4; Length 329;
Best Local Similarity 26.9%; Pred. No. 1.4e-19;
RESULT 423
ID ADM20140 standard; protein; 329 AA.
DE Protein encoded by novel human channel/transporter gene #218 clone 3.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 302.5; DB 4; Length 329;
Best Local Similarity 26.9%; Pred. No. 1.4e-19;
RESULT 424
ID ADM19900 standard; protein; 329 AA.
DE Protein encoded by novel human channel/transporter gene #218.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 302.5; DB 4; Length 329;
Best Local Similarity 26.9%; Pred. No. 1.4e-19;

RESULT 425
ID ADM19901 standard; protein; 329 AA.
DE Protein encoded by novel human channel/transporter gene #219.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 302.5; DB 4; Length 329;
Best Local Similarity 26.9%; Pred. No. 1.4e-19;
RESULT 426
ID AAM61169 standard; protein; 298 AA.
DE Anti protein.
PN WO9819714-A1.
PD 14-MAY-1998.
PA (UYEM-) UNIV EMORY.
Query Match 12.5%; Score 302; DB 2; Length 298;
Best Local Similarity 28.6%; Pred. No. 1.3e-19;
RESULT 427
ID AAY71032 standard; protein; 298 AA.
DE Human adenine nucleotide translocator ANT2.
PN WO200026370-A2.
PD 11-MAY-2000.
PA (MITO-) MITOKOR.
Query Match 12.5%; Score 302; DB 3; Length 298;
Best Local Similarity 29.1%; Pred. No. 1.3e-19;
RESULT 428
ID AAV01199 standard; protein; 298 AA.
DE Human adenine nucleotide translocator-2 (ANT2) protein.
PN WO200132876-A2.
PD 10-MAY-2001.
PA (MITO-) MITOKOR.
Query Match 12.5%; Score 302; DB 4; Length 298;
Best Local Similarity 29.1%; Pred. No. 1.3e-19;
RESULT 429
ID AAU10379 standard; protein; 298 AA.
DE Human adenine nucleotide translocator 2 (ANT2).
PN WO200185944-A2.
PD 15-NOV-2001.
PA (MITO-) MITOKOR.
Query Match 12.5%; Score 302; DB 5; Length 298;
Best Local Similarity 29.1%; Pred. No. 1.3e-19;
RESULT 430
ID APT89428 standard; protein; 298 AA.
DE Human adenine nucleotide translocator 2 (ANT2) protein.
PN US6797467-B1.
PD 28-SEP-2004.
PA (MITO-) MITOKOR.
Query Match 12.5%; Score 302; DB 8; Length 298;
Best Local Similarity 29.1%; Pred. No. 1.3e-19;
RESULT 431
ID AAB50382 standard; protein; 311 AA.
DE Human uncoupling protein #5.
PN WO200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.4%; Score 301.5; DB 3; Length 311;
Best Local Similarity 28.7%; Pred. No. 1.5e-19;
RESULT 432
ID AAM39173 standard; protein; 311 AA.
DE Human polypeptide SEQ ID NO 2318.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.4%; Score 301.5; DB 4; Length 311;
Best Local Similarity 28.7%; Pred. No. 1.5e-19;
RESULT 433
ID AEG76620 standard; protein; 316 AA.
DE Mouse SOUP1 protein.
PN WO200242455-A2.
PD 30-MAY-2002.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 12.4%; Score 301.5; DB 5; Length 316;
Best Local Similarity 31.4%; Pred. No. 1.6e-19;
RESULT 434

ID AAB51795 standard; protein; 335 AA.
DE Human secreted protein sequence encoded by gene 21 SRQ ID NO:124.
PN W020061625-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 12.4%; Score 301.5; DB 3; Length 335;
Best Local Similarity 26.9%; Pred. No. 1.7e-19;
RESULT 435
ID ABR41715 standard; protein; 429 AA.
DE Human DTHP organelle-associated protein.
PN W0200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.4%; Score 301.5; DB 6; Length 429;
Best Local Similarity 30.8%; Pred. No. 2.5e-19;
RESULT 436
ID ADJ11556 standard; protein; 677 AA.
DE Rice protein modulated by post-transcriptional gene silencing SeqID 192.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKS D.
Query Match 12.4%; Score 301; DB 7; Length 677;
Best Local Similarity 26.8%; Pred. No. 5.5e-19;
RESULT 437
ID AAG22077 standard; protein; 331 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24869.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 300; DB 3; Length 331;
Best Local Similarity 28.0%; Pred. No. 2.4e-19;
RESULT 438
ID AAM17054 standard; protein; 289 AA.
DE Blackcurrant RIB7 polypeptide.
PN W09717452-A1.
PD 15-MAY-1997.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 28.9%; Score 299.5; DB 2; Length 289;
Best Local Similarity 28.9%; Pred. No. 2.1e-19;
RESULT 439
ID AAG16974 standard; protein; 306 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17820.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 299.5; DB 3; Length 306;
Best Local Similarity 28.1%; Pred. No. 2.3e-19;
RESULT 440
ID AAG12916 standard; protein; 306 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12214.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.4%; Score 299.5; DB 3; Length 306;
Best Local Similarity 28.1%; Pred. No. 2.3e-19;
RESULT 441
ID AAE10324 standard; protein; 315 AA.
DE Human transporter and ion channel-1 (TRICH-1) protein.
PN W0200162823-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.4%; Score 299.5; DB 4; Length 315;
Best Local Similarity 30.7%; Pred. No. 2.4e-19;
RESULT 442
ID AAB94269 standard; protein; 315 AA.
DE Human protein sequence SEQ ID NO:14687.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.4%; Score 299.5; DB 4; Length 315;
Best Local Similarity 30.7%; Pred. No. 2.4e-19;
RESULT 443
ID AAB94664 standard; protein; 315 AA.
DE Human protein sequence SEQ ID NO:15590.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.4%; Score 299.5; DB 4; Length 315;
Best Local Similarity 30.7%; Pred. No. 2.4e-19;
RESULT 444
ID AAG76619 standard; protein; 315 AA.
DE Human SOD1 protein.
PN W0200242455-A2.
PD 30-MAY-2002.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 12.4%; Score 299.5; DB 5; Length 315;
Best Local Similarity 30.7%; Pred. No. 2.4e-19;
RESULT 445
ID AAG76621 standard; protein; 316 AA.
DE Mouse 6i protein.
PN W0200242455-A2.
PD 30-MAY-2002.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 12.4%; Score 299.5; DB 5; Length 316;
Best Local Similarity 31.4%; Pred. No. 2.4e-19;
RESULT 446
ID AAG47533 standard; protein; 307 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59922.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.3%; Score 299; DB 3; Length 307;
Best Local Similarity 30.6%; Pred. No. 2.6e-19;
RESULT 447
ID AAG47532 standard; protein; 317 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59921.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.3%; Score 299; DB 3; Length 317;
Best Local Similarity 30.6%; Pred. No. 2.7e-19;
RESULT 448
ID ABB63182 standard; protein; 303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 16338.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 12.3%; Score 298; DB 4; Length 303;
Best Local Similarity 27.6%; Pred. No. 3.2e-19;
RESULT 449
ID ABB71142 standard; protein; 358 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 40218.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 12.3%; Score 298; DB 4; Length 358;
Best Local Similarity 24.5%; Pred. No. 4.1e-19;
RESULT 450
ID ABB66634 standard; protein; 272 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 26694.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 12.3%; Score 297; DB 4; Length 272;
Best Local Similarity 42.5%; Pred. No. 3.4e-19;
RESULT 451
ID AAG12917 standard; protein; 291 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12215.
PN EP1033405-A2.

PD 06-SEP-2000.
Query Match 12.2%; Score 296.5; DB 3; Length 291;
Best Local Similarity 27.9%; Pred. No. 4.2e-19;
RESULT 452
ID MAG16975 standard; protein; 291 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17821.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.2%; Score 296.5; DB 3; Length 291;
Best Local Similarity 27.9%; Pred. No. 4.2e-19;
RESULT 453
ID ADN21360 standard; protein; 283 AA.
DE Bacterial polypeptide #4013.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.2%; Score 295.5; DB 8; Length 283;
Best Local Similarity 27.9%; Pred. No. 5e-19;
RESULT 454
ID ABB66082 standard; protein; 299 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25038.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 295.5; DB 4; Length 299;
Best Local Similarity 27.9%; Pred. No. 5.4e-19;
RESULT 455
ID ABB67300 standard; protein; 299 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28692.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 295.5; DB 4; Length 299;
Best Local Similarity 27.9%; Pred. No. 5.4e-19;
RESULT 456
ID ADS96530 standard; protein; 299 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 151.
PN WO2004038999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 295.5; DB 8; Length 299;
Best Local Similarity 27.9%; Pred. No. 5.4e-19;
RESULT 457
ID ABB58380 standard; protein; 307 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1932.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.2%; Score 295.5; DB 4; Length 307;
Best Local Similarity 26.0%; Pred. No. 5.6e-19;
RESULT 458
ID AAB93001 standard; protein; 310 AA.
DE Human protein sequence SEQ ID NO:11741.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.2%; Score 295; DB 4; Length 310;
Best Local Similarity 28.4%; Pred. No. 6.3e-19;
RESULT 459
ID ABG70178 standard; protein; 310 AA.
DE Human prey protein for Shigella ipan9.8 #8.
PN WO200257303-A2.
PD 25-JUL-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 12.2%; Score 295; DB 5; Length 310;
Best Local Similarity 28.4%; Pred. No. 6.3e-19;
RESULT 460
ID ADN03795 standard; protein; 310 AA.
DE Antiporiatic protein sequence #94.
PD 06-SEP-2000.
Query Match 12.2%; Score 293.5; DB 3; Length 312;
Best Local Similarity 29.8%; Pred. No. 8.9e-19;
RESULT 461
ID MAG23665 standard; protein; 312 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27057.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.1%; Score 293.5; DB 3; Length 312;
Best Local Similarity 29.8%; Pred. No. 8.9e-19;
RESULT 462
ID ADN74667 standard; protein; 312 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SegID 2562.
PN WO2004035798-A2.
PD 29-APR-2004
PA (CROP-) CROPDESIGN NV.
Query Match 12.1%; Score 293.5; DB 8; Length 312;
Best Local Similarity 29.8%; Pred. No. 8.9e-19;
RESULT 463
ID ADN23463 standard; protein; 306 AA.
DE Bacterial polypeptide #6116.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.1%; Score 293; DB 8; Length 306;
Best Local Similarity 27.4%; Pred. No. 9.6e-19;
RESULT 464
ID AAG20658 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22935.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.0%; Score 291.5; DB 3; Length 330;
Best Local Similarity 28.0%; Pred. No. 1.5e-18;
RESULT 465
ID AAG3398 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48742.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 12.0%; Score 290.5; DB 3; Length 330;
Best Local Similarity 28.0%; Pred. No. 1.9e-18;
RESULT 466
ID ADB70116 standard; protein; 349 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3160.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.0%; Score 290.5; DB 7; Length 349;
Best Local Similarity 28.6%; Pred. No. 2e-18;
RESULT 467
ID ABG76618 standard; protein; 304 AA.
DE Fruit fly GH22139 protein sequence.
PN WO200242455-A2.
PD 30-MAY-2002
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 11.9%; Score 289; DB 5; Length 304;
Best Local Similarity 28.9%; Pred. No. 2.3e-18;
RESULT 468
ID AAY94666 standard; protein; 322 AA.
DE Human uncoupling protein isoform hUCP5 amino acid sequence.
PN WO200032624-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 11.9%; Score 289; DB 3; Length 322;
Best Local Similarity 29.3%; Pred. No. 2.5e-18;
RESULT 469
ID AAM85008 standard; protein; 280 AA.
DE Human diagnostic and therapeutic pproetin SEQ ID NO:5257.

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PA	(HYSE-) HYSEQ INC.	11.8%;	Score 286.5;	DB 4;	Length 325;
Query Match					
Best Local Similarity		28.1%;	Pred. No. 4.3e-18;		
RESULT 479					
ID	AAV94665 standard; protein; 325 AA.				
DE	Human uncoupling protein (UCP5) amino acid sequence.				
PN	WO200032624-A2.				
PD	08-JUN-2000.				
PA	(GETH-) GENENTECH INC.				
Query Match		11.8%;	Score 286;	DB 3;	Length 325;
Best Local Similarity		29.7%;	Pred. No. 4.8e-18;		
RESULT 480					
ID	AAE60656 standard; protein; 334 AA.				
DE	Human gene 16 encoded secreted protein HMTAP86, SEQ ID NO:118.				
PN	WO200151504-A1.				
PD	19-JUL-2001.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
Query Match		11.8%;	Score 286;	DB 4;	Length 334;
Best Local Similarity		29.7%;	Pred. No. 5.1e-18;		
RESULT 481					
ID	ABG33878 standard; protein; 334 AA.				
DE	Human secreted protein encoded by gene 16.				
PN	WO200226931-A2.				
PD	04-APR-2002.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
Query Match		11.8%;	Score 286;	DB 5;	Length 334;
Best Local Similarity		29.7%;	Pred. No. 5.1e-18;		
RESULT 482					
ID	ADA57046 standard; protein; 334 AA.				
DE	Human secreted protein #329.				
PN	WO2002102994-A2.				
PD	27-DEC-2002.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
Query Match		11.8%;	Score 286;	DB 6;	Length 334;
Best Local Similarity		29.7%;	Pred. No. 5.1e-18;		
RESULT 483					
ID	ADA40900 standard; protein; 334 AA.				
DE	Human secreted protein.				
PN	WO2002102993-A2.				
PD	27-DEC-2002.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
Query Match		11.8%;	Score 286;	DB 6;	Length 334;
Best Local Similarity		29.7%;	Pred. No. 5.1e-18;		
RESULT 484					
ID	AAV87079 standard; protein; 335 AA.				
DE	Human secreted protein sequence SEQ ID NO:118.				
PN	WO200004140-A1.				
PD	27-JAN-2000.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
Query Match		11.8%;	Score 286;	DB 3;	Length 335;
Best Local Similarity		29.7%;	Pred. No. 5.1e-18;		
RESULT 485					
ID	AAV94668 standard; protein; 322 AA.				
DE	Murine uncoupling protein isoform mUCP5L amino acid sequence.				
PN	WO200032624-A2.				
PD	08-JUN-2000.				
PA	(GETH-) GENENTECH INC.				
Query Match		11.8%;	Score 285;	DB 3;	Length 322;
Best Local Similarity		30.1%;	Pred. No. 5.9e-18;		
RESULT 486					
ID	AAV94669 standard; protein; 325 AA.				
DE	Murine uncoupling protein isoform mUCP5S amino acid sequence.				
PN	WO200032624-A2.				
PD	08-JUN-2000.				
PA	(GETH-) GENENTECH INC.				
Query Match		11.8%;	Score 285;	DB 3;	Length 325;
Best Local Similarity		30.1%;	Pred. No. 6e-18;		
RESULT 487					
ID	ADG23325 standard; protein; 294 AA.				
DE	Bacterial polypeptide #12356.				
PN	US2003233675-A1.				
PD	18-DEC-2003.				
PA	(CAOY/) CAO Y.				

PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 11.7%; Score 284.5; DB 8; Length 294;
Best Local Similarity 28.6%; Pred. No. 5.8e-18;
RESULT 488
ID AAG14091 standard; protein; 285 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13823.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.7%; Score 284; DB 3; Length 285;
Best Local Similarity 30.2%; Pred. No. 6.2e-18;
RESULT 489
ID AEM83905 standard; protein; 303 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4154.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 284; DB 8; Length 303;
Best Local Similarity 26.6%; Pred. No. 6.8e-18;
RESULT 490
ID AEM83907 standard; protein; 303 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4156.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 284; DB 8; Length 303;
Best Local Similarity 26.6%; Pred. No. 6.8e-18;
RESULT 491
ID AEM83903 standard; protein; 303 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4152.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 284; DB 8; Length 303;
Best Local Similarity 26.6%; Pred. No. 6.8e-18;
RESULT 492
ID AEM83904 standard; protein; 303 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4153.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 284; DB 8; Length 303;
Best Local Similarity 26.6%; Pred. No. 6.8e-18;
RESULT 493
ID AEM83909 standard; protein; 303 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4158.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 284; DB 8; Length 303;
Best Local Similarity 26.6%; Pred. No. 6.8e-18;
RESULT 494
ID AEM83908 standard; protein; 303 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4157.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 284; DB 8; Length 303;
Best Local Similarity 26.6%; Pred. No. 6.8e-18;
RESULT 495
ID ADA05792 standard; protein; 325 AA.
DE Human NOV35e protein SEQ ID NO:152.
PN W02003028424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 11.7%; Score 283; DB 6; Length 325;
Best Local Similarity 29.4%; Pred. No. 9.3e-18;
RESULT 496
ID ABP73346 standard; protein; 399 AA.
DE Candida albicans essential protein SEQ ID NO 7183.
PN W0200253728-A2.

PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.6%; Score 282; DB 5; Length 399;
Best Local Similarity 28.8%; Pred. No. 1.6e-17;
RESULT 497
ID AAG22078 standard; protein; 290 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24870.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.6%; Score 281.5; DB 3; Length 290;
Best Local Similarity 29.6%; Pred. No. 1.1e-17;
RESULT 498
ID ADS43770 standard; protein; 322 AA.
DE Bacterial polypeptide #22200.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 11.6%; Score 280; DB 8; Length 322;
Best Local Similarity 28.5%; Pred. No. 1.8e-17;
RESULT 499
ID ADN62956 standard; protein; 325 AA.
DE Human NOV35e.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILT/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJ/) JU J.
PA (LIL/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CAT/) CATTERTON E.
PA (JIM/) JI W.
PA (MILT/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PEN/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 11.6%; Score 280; DB 8; Length 325;
Best Local Similarity 29.4%; Pred. No. 1.8e-17;
RESULT 500
ID ADS23620 standard; protein; 386 AA.
DE Bacterial polypeptide #12653.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S. 11.6%; Score 280; DB 8; Length 386;
Query Match
Best Local Similarity 25.4%; Pred. No. 2.3e-17;
RESULT 501
ID AAG20659 standard; protein; 291 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22936.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 11.5%; Score 279.5; DB 3; Length 291;
RESULT 502
ID ABG76658 standard; protein; 324 AA.
DE Zebrafish SOUP1 protein.
PN WC200242455-A2.
PD 30-MAY-2002.
PA (DBVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match
Best Local Similarity 11.5%; Score 279; DB 5; Length 324;
RESULT 503
ID AAG47534 standard; protein; 284 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59923.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 11.5%; Score 278.5; DB 3; Length 284;
RESULT 504
ID AAG39399 standard; protein; 291 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48743.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 11.5%; Score 278.5; DB 3; Length 291;
RESULT 505
ID ADN23419 standard; protein; 313 AA.
DE Bacterial polypeptide #6072.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.5%; Score 277.5; DB 8; Length 313;
RESULT 506
ID ADN23450 standard; protein; 313 AA.
DE Bacterial polypeptide #6103.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.5%; Score 277.5; DB 8; Length 313;
RESULT 507
ID ADS43545 standard; protein; 314 AA.
DE Bacterial polypeptide #21975.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.5%; Score 277.5; DB 8; Length 314;
RESULT 508
ID AAY78511 standard; protein; 290 AA.
DE Human uncoupling protein 4 (UCP-4) amino acid sequence.
PN WC200004037-A1.
PD 27-JUN-2000.

PA (AMYL-) AMYLIN PHARM INC. 11.4%; Score 277; DB 3; Length 290;
Query Match
Best Local Similarity 29.6%; Pred. No. 2.9e-17;
RESULT 509
ID ADS43686 standard; protein; 373 AA.
DE Bacterial polypeptide #22116.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.3%; Score 275; DB 8; Length 373;
RESULT 510
ID ADN22435 standard; protein; 300 AA.
DE Bacterial polypeptide #5088.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.3%; Score 274; DB 8; Length 300;
RESULT 511
ID ADN19068 standard; protein; 335 AA.
DE Bacterial polypeptide #1721.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.3%; Score 274; DB 8; Length 335;
RESULT 512
ID ADN19761 standard; protein; 277 AA.
DE Bacterial polypeptide #2414.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.3%; Score 273.5; DB 8; Length 277;
RESULT 513
ID ADN19769 standard; protein; 277 AA.
DE Bacterial polypeptide #2422.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 11.3%; Score 273.5; DB 8; Length 277;
RESULT 514
ID AAM99654 standard; protein; 678 AA.
DE Human adenosine nucleotide translocator 4.
PN WC9907845-A1.
PD 18-FEB-1999.
PA (SMIK-) SMITHKLINE BEECHAM LAB PHARM.
Query Match
Best Local Similarity 11.2%; Score 272.5; DB 2; Length 678;
RESULT 515
ID ADN23266 standard; protein; 300 AA.

DE Bacterial polypeptide #5919.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
DE (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 11.2%; Score 270.5; DB 8; Length 300;
Best Local Similarity 27.4%; Pred. No. 1.3e-16;
RESULT 516
ID AAB94292 standard; protein; 678 AA.
DE Human protein sequence SEQ ID NO:14741.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELT-) HELIX RES INST.
Query Match 11.2%; Score 270.5; DB 4; Length 678;
Best Local Similarity 21.7%; Pred. No. 4.3e-16;
RESULT 517
ID AA018517 standard; protein; 678 AA.
DE Human insulin receptor signaling modifier SEQ ID NO: 56.
PN WO200255664-A2.
PD 18-JUL-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 11.2%; Score 270.5; DB 5; Length 678;
Best Local Similarity 21.7%; Pred. No. 4.3e-16;
RESULT 518
ID A070251 standard; protein; 678 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID2057.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 11.2%; Score 270.5; DB 7; Length 678;
Best Local Similarity 21.7%; Pred. No. 4.3e-16;
RESULT 519
ID A066893 standard; protein; 678 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID499.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 11.2%; Score 270.5; DB 7; Length 678;
Best Local Similarity 21.7%; Pred. No. 4.3e-16;
RESULT 520
ID AAM39247 standard; protein; 680 AA.
DE Human polypeptide SEQ ID NO 2392.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.2%; Score 270.5; DB 4; Length 680;
Best Local Similarity 21.7%; Pred. No. 4.3e-16;
RESULT 521
ID AAU28170 standard; protein; 680 AA.
DE Novel human secretory protein, Seq ID No 339.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.2%; Score 270.5; DB 4; Length 680;
Best Local Similarity 21.7%; Pred. No. 4.3e-16;
RESULT 522
ID AAM43653 standard; protein; 684 AA.
DE Human polypeptide SEQ ID NO 331.
PN WO200155308-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.2%; Score 270.5; DB 4; Length 684;
Best Local Similarity 21.7%; Pred. No. 4.4e-16;
RESULT 523
ID AAU87679 standard; protein; 684 AA.
DE Novel central nervous system protein #589.
PN WO200155318-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.2%; Score 270.5; DB 4; Length 684;
Best Local Similarity 21.7%; Pred. No. 4.4e-16;
RESULT 524
ID AD154994 standard; protein; 684 AA.
DE Novel human protein seq id 1197.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 11.2%; Score 270.5; DB 8; Length 684;
Best Local Similarity 21.7%; Pred. No. 4.4e-16;
RESULT 525
ID ADM24674 standard; protein; 684 AA.
DE Human PRO polypeptide #157.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.2%; Score 270.5; DB 8; Length 684;
Best Local Similarity 21.7%; Pred. No. 4.4e-16;
RESULT 526
ID AAM41033 standard; protein; 713 AA.
DE Human polypeptide SEQ ID NO 5964.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.2%; Score 270.5; DB 4; Length 713;
Best Local Similarity 22.4%; Pred. No. 4.6e-16;
RESULT 527
ID ABB61130 standard; protein; 379 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10182.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 11.1%; Score 269; DB 4; Length 379;
Best Local Similarity 28.7%; Pred. No. 2.5e-16;
RESULT 528
ID AAY13036 standard; protein; 125 AA.
DE Human secreted protein encoded by 5' EST SEQ ID NO: 50.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 11.1%; Score 268; DB 2; Length 125;
Best Local Similarity 92.9%; Pred. No. 5.9e-17;
RESULT 529
ID AAY94667 standard; protein; 353 AA.
DE Human uncoupling protein isoform hUCP51 amino acid sequence.
PN WO200032624-A2.
PD 08-JUN-2000.
PA (GENT-) GENENTECH INC.
Query Match 11.0%; Score 266.5; DB 3; Length 353;
Best Local Similarity 27.1%; Pred. No. 3.9e-16;
RESULT 530
ID AAM41290 standard; protein; 272 AA.
DE Human polypeptide SEQ ID NO 6221.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.0%; Score 266; DB 4; Length 272;
Best Local Similarity 31.3%; Pred. No. 2.9e-16;
RESULT 531
ID ABJ25394 standard; protein; 313 AA.
DE Aspergillus fumigatus essential gene protein #52.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.0%; Score 266; DB 6; Length 313;
Best Local Similarity 25.7%; Pred. No. 3.6e-16;
RESULT 532
ID AAG43094 standard; protein; 278 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53822.
PN EP1033405-A2.

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PD 06-SEP-2000.
Query Match 11.0%; Score 265.5; DB 3; Length 278;
Best Local Similarity 29.5%; Pred. No. 3.4e-16;
RESULT 533
ID AAY90322 standard; protein; 291 AA.
DE Novel human protein sequence #1.
PD WO200047617-A1.
PD 17-AUG-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 11.0%; Score 265.5; DB 3; Length 291;
Best Local Similarity 28.3%; Pred. No. 3.6e-16;
RESULT 534
ID ADN20861 standard; protein; 391 AA.
DE Bacterial polypeptide #3514.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.9%; Score 264.5; DB 8; Length 391;
Best Local Similarity 24.7%; Pred. No. 7e-16;
RESULT 535
ID ADS43847 standard; protein; 304 AA.
DE Bacterial polypeptide #22277.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.9%; Score 263; DB 8; Length 304;
Best Local Similarity 28.1%; Pred. No. 6.6e-16;
RESULT 536
ID ADS23656 standard; protein; 336 AA.
DE Bacterial polypeptide #12689.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.8%; Score 262; DB 8; Length 336;
Best Local Similarity 24.9%; Pred. No. 9.6e-16;
RESULT 537
ID AAO16518 standard; protein; 674 AA.
DE Human insulin receptor signaling modifier SEQ ID NO: 58.
PD WO200255664-A2.
PD 18-JUL-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 10.8%; Score 261.5; DB 5; Length 674;
Best Local Similarity 23.4%; Pred. No. 3e-15;
RESULT 538
ID ADJ69046 standard; protein; 675 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID852.
PD WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 10.8%; Score 261.5; DB 7; Length 675;
Best Local Similarity 23.4%; Pred. No. 3e-15;
RESULT 539
ID ADP23606 standard; protein; 675 AA.
DE PRO polypeptide SEQ ID NO:784.
PD WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 10.8%; Score 261.5; DB 8; Length 675;
Best Local Similarity 23.4%; Pred. No. 3e-15;
RESULT 540
ID ADN23777 standard; protein; 343 AA.
DE Bacterial polypeptide #6430.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.8%; Score 261; DB 8; Length 343;
Best Local Similarity 26.5%; Pred. No. 1.2e-15;
RESULT 541
ID AAY05712 standard; protein; 674 AA.
DE Human adenine nucleotide translocator ANTS.
PD EP911341-A1.
PD 28-APR-1999.
PA (SMIK-) SMITHKLINE BEECHAM LAB PHARM.
Query Match 10.8%; Score 261; DB 2; Length 674;
Best Local Similarity 23.4%; Pred. No. 3.4e-15;
RESULT 542
ID AAY1934 standard; protein; 174 AA.
DE Soybean brittle-1 partial polypeptide.
PD WO9949047-A2.
PD 30-SEP-1999.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 10.8%; Score 260.5; DB 2; Length 174;
Best Local Similarity 32.9%; Pred. No. 4.9e-16;
RESULT 543
ID AAG06092 standard; protein; 243 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 2739.
PD EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 259.5; DB 3; Length 243;
Best Local Similarity 28.8%; Pred. No. 1e-15;
RESULT 544
ID ADS43658 standard; protein; 311 AA.
DE Bacterial polypeptide #22088.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.7%; Score 259; DB 8; Length 311;
Best Local Similarity 28.5%; Pred. No. 1.6e-15;
RESULT 545
ID ABB58893 standard; protein; 643 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3471.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.7%; Score 259; DB 4; Length 643;
Best Local Similarity 21.3%; Pred. No. 4.9e-15;
RESULT 546
ID ABB58691 standard; protein; 682 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3465.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.7%; Score 259; DB 4; Length 682;
Best Local Similarity 21.3%; Pred. No. 5.3e-15;
RESULT 547
ID ABB58765 standard; protein; 695 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3087.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.7%; Score 259; DB 4; Length 695;
Best Local Similarity 21.3%; Pred. No. 5.5e-15;
RESULT 548
ID AAB43247 standard; protein; 708 AA.
DE Human ORFX ORF3011 polypeptide sequence SRQ ID NO:6022.
```

PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.7%; Score 259; DB 3; Length 708;
Best Local Similarity 23.5%; Pred. No. 5.6e-15;
RESULT 549
ID AAG2079 standard; protein; 278 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24871.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.7%; Score 258.5; DB 3; Length 278;
Best Local Similarity 29.1%; Pred. No. 1.5e-15;
RESULT 550
ID ADN24356 standard; protein; 300 AA.
DE Bacterial polypeptide #7009.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.6%; Score 258; DB 8; Length 300;
Best Local Similarity 28.3%; Pred. No. 1.9e-15;
RESULT 551
ID AAG2818 standard; protein; 312 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33314.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.6%; Score 257.5; DB 3; Length 312;
Best Local Similarity 29.9%; Pred. No. 2.3e-15;
RESULT 552
ID AAM00938 standard; protein; 366 AA.
DE Human bone marrow protein, SEQ ID NO: 414.
PN W0200153453-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 257; DB 4; Length 366;
Best Local Similarity 25.8%; Pred. No. 3.2e-15;
RESULT 553
ID AAM83177 standard; protein; 261 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5426.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.6%; Score 256.5; DB 8; Length 261;
Best Local Similarity 27.1%; Pred. No. 2.2e-15;
RESULT 554
ID ADM03791 standard; protein; 291 AA.
DE Human protein of the invention SEQ ID NO:2476.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.6%; Score 256.5; DB 7; Length 291;
Best Local Similarity 28.0%; Pred. No. 2.6e-15;
RESULT 555
ID AAG40397 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50119.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.6%; Score 256.5; DB 3; Length 305;
Best Local Similarity 26.8%; Pred. No. 2.7e-15;
RESULT 556
ID AAG23372 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26655.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.6%; Score 256.5; DB 3; Length 305;
Best Local Similarity 26.8%; Pred. No. 2.7e-15;
RESULT 557
ID AAG16976 standard; protein; 263 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17822.
PN EP1033405-A2.

PD 06-SEP-2000.
Query Match 10.6%; Score 256; DB 3; Length 263;
Best Local Similarity 28.3%; Pred. No. 2.5e-15;
RESULT 558
ID AAG12918 standard; protein; 263 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12216.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.6%; Score 256; DB 3; Length 263;
Best Local Similarity 28.3%; Pred. No. 2.5e-15;
RESULT 559
ID ADC3192 standard; protein; 293 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 134.
PN W02003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.6%; Score 256; DB 7; Length 293;
Best Local Similarity 27.4%; Pred. No. 2.9e-15;
RESULT 560
ID ADA22671 standard; protein; 267 AA.
DE A. gosypii transport protein fragment from Oligo 163 SEQ ID 15.
PN W02003014353-A2.
PD 20-FEB-2003.
PA (BADT-) BASF AG.
Query Match 10.5%; Score 255.5; DB 6; Length 267;
Best Local Similarity 29.3%; Pred. No. 2.8e-15;
RESULT 561
ID ABM83485 standard; protein; 364 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3734.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.5%; Score 255.5; DB 8; Length 364;
Best Local Similarity 28.0%; Pred. No. 4.5e-15;
RESULT 562
ID AAG40398 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50120.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.5%; Score 255; DB 3; Length 282;
Best Local Similarity 26.1%; Pred. No. 3.4e-15;
RESULT 563
ID AAG23373 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26656.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.5%; Score 255; DB 3; Length 282;
Best Local Similarity 26.1%; Pred. No. 3.4e-15;
RESULT 564
ID ABB90361 standard; protein; 321 AA.
DE Human polypeptide SEQ ID NO 2737.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HOMA-) HUMAN GENOME SCI INC.
Query Match 10.5%; Score 255; DB 5; Length 321;
Best Local Similarity 24.1%; Pred. No. 4.1e-15;
RESULT 565
ID ABB91591 standard; protein; 367 AA.
DE Herbicidally active polypeptide SEQ ID NO 802.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB-) BAYER AG.
Query Match 10.5%; Score 254.5; DB 5; Length 367;
Best Local Similarity 26.3%; Pred. No. 5.6e-15;
RESULT 566
ID AAM93465 standard; protein; 314 AA.
DE Human polypeptide, SEQ ID NO: 3130.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELT-) HELIX RES INST.
Query Match 10.5%; Score 254; DB 4; Length 314;
Best Local Similarity 24.1%; Pred. No. 5e-15;
RESULT 567

ID AAM93824 standard; protein; 314 AA.
DE Human polypeptide, SEQ ID NO: 3883.
PN EPI30094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.5%; Score 254; DB 4; Length 314;
Best Local Similarity 24.1%; Pred. No. 5e-15;
RESULT 568
ID ADJ70271 standard; protein; 314 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2077.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 10.5%; Score 254; DB 7; Length 314;
Best Local Similarity 24.1%; Pred. No. 5e-15;
RESULT 569
ID ADJ31097 standard; protein; 314 AA.
DE Human protein encoded by a full length cDNA clone SegID 3130.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.5%; Score 254; DB 8; Length 314;
Best Local Similarity 24.1%; Pred. No. 5e-15;
RESULT 570
ID ADJ31850 standard; protein; 314 AA.
DE Human protein encoded by a full length cDNA clone SegID 3883.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.5%; Score 254; DB 8; Length 314;
Best Local Similarity 24.1%; Pred. No. 5e-15;
RESULT 571
ID ADQ1294 standard; protein; 368 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2113.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.5%; Score 254; DB 8; Length 368;
Best Local Similarity 24.1%; Pred. No. 6.3e-15;
RESULT 572
ID AAM41505 standard; protein; 318 AA.
DE Human polypeptide SEQ ID NO 6436.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.5%; Score 253.5; DB 4; Length 318;
Best Local Similarity 28.3%; Pred. No. 5.6e-15;
RESULT 573
ID ADC33155 standard; protein; 318 AA.
DE Human novel config-encoded polypeptide sequence, SEQ ID NO:3237.
PN WO2003028271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.5%; Score 253.5; DB 7; Length 318;
Best Local Similarity 28.3%; Pred. No. 5.6e-15;
RESULT 574
ID ABM83484 standard; protein; 376 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3733.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.5%; Score 253.5; DB 8; Length 376;
Best Local Similarity 28.3%; Pred. No. 7.2e-15;
RESULT 575
ID ADB64246 standard; protein; 256 AA.
DE Human protein encoded by clone DFNES20057660.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.4%; Score 253; DB 7; Length 256;
Best Local Similarity 29.7%; Pred. No. 4.5e-15;

RESULT 576
ID ABP43205 standard; protein; 228 AA.
DE Human ovarian antigen HVDN29, SEQ ID NO:4337.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 252; DB 5; Length 228;
Best Local Similarity 33.7%; Pred. No. 4.7e-15;
RESULT 577
ID AAG16697 standard; protein; 285 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17443.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (GOLD/) GOLDMAN B S.
Query Match 10.4%; Score 251; DB 3; Length 285;
Best Local Similarity 27.8%; Pred. No. 8.2e-15;
RESULT 578
ID ADS43716 standard; protein; 314 AA.
DE Bacterial polypeptide #22146.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.4%; Score 251; DB 8; Length 314;
Best Local Similarity 26.4%; Pred. No. 9.5e-15;
RESULT 579
ID AAM39174 standard; protein; 285 AA.
DE Human polypeptide SEQ ID NO 2319.
PN WO200153312-A1.
PD 26-JUN-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 250.5; DB 4; Length 285;
Best Local Similarity 27.7%; Pred. No. 9.2e-15;
RESULT 580
ID AAG28189 standard; protein; 228 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33315.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 250; DB 3; Length 228;
Best Local Similarity 31.0%; Pred. No. 7.3e-15;
RESULT 581
ID ADJ76347 standard; protein; 309 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1599.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 10.2%; Score 247; DB 8; Length 309;
Best Local Similarity 27.0%; Pred. No. 2.2e-14;
RESULT 582
ID ABM82796 standard; protein; 344 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3045.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.2%; Score 247; DB 8; Length 344;
Best Local Similarity 25.3%; Pred. No. 2.6e-14;
RESULT 583
ID ABB59263 standard; protein; 449 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 4581.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.2%; Score 247; DB 4; Length 449;
Best Local Similarity 25.8%; Pred. No. 3.9e-14;
RESULT 584
ID AAG28051 standard; protein; 459 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33123.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (GOLD/) GOLDMAN B S.
Query Match 10.2%; Score 246.5; DB 3; Length 459;
Best Local Similarity 28.1%; Pred. No. 4.5e-14;

RESULT 585
ID AAG28050 standard; protein; 502 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33122.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 246.5; DB 3; Length 502;
Best Local Similarity 28.1%; Pred. No. 5.1e-14;
RESULT 586
ID AAG28049 standard; protein; 617 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33121.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.2%; Score 246.5; DB 3; Length 617;
Best Local Similarity 28.1%; Pred. No. 7e-14;
RESULT 587
ID ADQ97539 standard; protein; 338 AA.
DE Human cancer associated sequence H909-010, SEQ ID 516.
PN WO2004050304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 246; DB 8; Length 338;
Best Local Similarity 25.0%; Pred. No. 3.2e-14;
RESULT 588
ID AAB50383 standard; protein; 289 AA.
DE Human uncoupling protein #6.
PN WO200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.1%; Score 245.5; DB 3; Length 289;
Best Local Similarity 28.1%; Pred. No. 2.8e-14;
RESULT 589
ID AAB60113 standard; protein; 289 AA.
DE Human transport protein TPPT-33.
PN WO200078953-A2.
PD 28-DEC-2000.
PA (INCYTE) INCYTE GENOMICS INC.
Query Match 10.1%; Score 245.5; DB 4; Length 289;
Best Local Similarity 28.1%; Pred. No. 2.8e-14;
RESULT 590
ID AAG39526 standard; protein; 300 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48919.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 300;
Best Local Similarity 25.4%; Pred. No. 3e-14;
RESULT 591
ID AAG1086 standard; protein; 300 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12448.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 300;
Best Local Similarity 25.4%; Pred. No. 3e-14;
RESULT 592
ID AAG37830 standard; protein; 300 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46581.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 300;
Best Local Similarity 25.4%; Pred. No. 3e-14;
RESULT 593
ID ADN74437 standard; protein; 300 AA.
DE Thale cress protein repressed in E2Fp/Dpa expressing plants SeqID 2332.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDISEIGN NV
Query Match 10.1%; Score 245.5; DB 8; Length 300;
Best Local Similarity 25.4%; Pred. No. 3e-14;
RESULT 594
ID AAG52781 standard; protein; 301 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67132.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 301;

Best Local Similarity 27.9%; Pred. No. 3e-14;
RESULT 595
ID AAG52783 standard; protein; 301 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67135.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 301;
Best Local Similarity 27.9%; Pred. No. 3e-14;
RESULT 596
ID AAG52780 standard; protein; 325 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67131.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 325;
Best Local Similarity 27.9%; Pred. No. 3.3e-14;
RESULT 597
ID AAG52782 standard; protein; 325 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67134.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 325;
Best Local Similarity 27.9%; Pred. No. 3.3e-14;
RESULT 598
ID AAG52779 standard; protein; 361 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67130.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.1%; Score 245.5; DB 3; Length 361;
Best Local Similarity 27.9%; Pred. No. 3.9e-14;
RESULT 599
ID AAM69166 standard; protein; 309 AA.
DE Human reepirator uncoupling protein-2 (UCP2).
PN WO9831396-A1.
PD 23-JUL-1998.
PA (UYDU-) UNIV DUKE.
PA (REGC) UNIV CALIFORNIA.
PA (CNRS) CENT NAT RECH SCI.
Query Match 10.1%; Score 245; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 3.4e-14;
RESULT 600
ID AAY28352 standard; protein; 309 AA.
DE UCP2 amino acid sequence (Fleury variant).
PN WO937812-A1.
PD 29-JUL-1999.
PA (ORCH-) ORCHID BIOCOMPUTER INC.
Query Match 10.1%; Score 245; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 3.4e-14;
RESULT 601
ID AAU98901 standard; protein; 309 AA.
DE Human uncoupling protein UCP-2.
PN WO200236829-A2.
PD 10-MAY-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 10.1%; Score 245; DB 5; Length 309;
Best Local Similarity 26.6%; Pred. No. 3.4e-14;
RESULT 602
ID ADG65407 standard; protein; 309 AA.
DE Human uncoupling protein 2 (UCP2).
PN US2003207284-A1.
PD 06-NOV-2003.
PA (CHEW/) CHEW A.
PA (DENT/) DENTON R R.
PA (GILS/) GILSON C R.
PA (NAND/) NANDABALAN K.
PA (PARK/) PARKS K E.
Query Match 10.1%; Score 245; DB 8; Length 309;
Best Local Similarity 26.6%; Pred. No. 3.4e-14;
RESULT 603
ID ADJ68206 standard; protein; 262 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID12.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 10.1%; Score 244.5; DB 7; Length 262;
Best Local Similarity 28.3%; Pred. No. 3e-14;
RESULT 604
ID AAB62523 standard; protein; 332 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14361.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 10.1%; Score 244.5; DB 4; Length 332;
Best Local Similarity 25.8%; Pred. No. 4.3e-14;
RESULT 605
ID ADE54389 standard; protein; 309 AA.
DE Rat protein P56500, SEQ ID NO 192.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 10.1%; Score 244; DB 7; Length 309;
Best Local Similarity 26.2%; Pred. No. 4.3e-14;
RESULT 606
ID AAM83487 standard; protein; 356 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3736.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.0%; Score 243.5; DB 8; Length 356;
Best Local Similarity 26.9%; Pred. No. 5.9e-14;
RESULT 607
ID ABA43205 standard; peptide; 56 AA.
DE Peptide #10711 encoded by human foetal liver single exon probe.
PN W0200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.0%; Score 243; DB 4; Length 56;
Best Local Similarity 80.4%; Pred. No. 4.1e-15;
RESULT 608
ID AAM37045 standard; protein; 56 AA.
DE Peptide #11082 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.0%; Score 243; DB 4; Length 56;
Best Local Similarity 80.4%; Pred. No. 4.1e-15;
RESULT 609
ID AAM76937 standard; protein; 56 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37243.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.0%; Score 243; DB 4; Length 56;
Best Local Similarity 80.4%; Pred. No. 4.1e-15;
RESULT 610
ID AAM6411 standard; protein; 56 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36216.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.0%; Score 243; DB 4; Length 56;
Best Local Similarity 80.4%; Pred. No. 4.1e-15;
RESULT 611
ID AAG58598 standard; peptide; 56 AA.
DE Human liver peptide, SEQ ID NO 37246.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.0%; Score 243; DB 4; Length 56;
Best Local Similarity 80.4%; Pred. No. 4.1e-15;
RESULT 612
ID AAG46046 standard; peptide; 56 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35711.
PN W0200186003-A2.
PD 15-NOV-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.0%; Score 243; DB 5; Length 56;
Best Local Similarity 80.4%; Pred. No. 4.1e-15;
RESULT 613
ID AAG22636 standard; protein; 374 AA.
DE Novel human diagnostic protein #22627.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 243; DB 4; Length 374;
Best Local Similarity 33.2%; Pred. No. 7.1e-14;
RESULT 614
ID AAB84827 standard; protein; 287 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5076.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.0%; Score 242.5; DB 8; Length 287;
Best Local Similarity 25.6%; Pred. No. 5.3e-14;
RESULT 615
ID ADC39188 standard; protein; 298 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 130.
PN W02003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 242; DB 7; Length 298;
Best Local Similarity 25.7%; Pred. No. 6.3e-14;
RESULT 616
ID ADQ66016 standard; protein; 303 AA.
DE Novel human protein sequence #989.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.0%; Score 242; DB 8; Length 303;
Best Local Similarity 28.4%; Pred. No. 6.4e-14;
RESULT 617
ID AAM24000 standard; protein; 309 AA.
DE Complete chimeric mouse/human C5 gene product.
PN US5702902-A.
PD 30-DEC-1997.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.0%; Score 242; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 618
ID AAM89546 standard; protein; 309 AA.
DE Full length human C5 protein sequence.
PN US5853975-A.
PD 29-DEC-1998.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.0%; Score 242; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 619
ID AAY28351 standard; protein; 309 AA.
DE UCP2 amino acid sequence.
PN W09937812-A1.
PD 29-JUL-1999.
PA (ORCH-) ORCHID BIOCOMPUTER INC.
Query Match 10.0%; Score 242; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 620
ID AAY28353 standard; protein; 309 AA.
DE UCP2 amino acid sequence (Gluteno variant).
PN W09937812-A1.
PD 29-JUL-1999.
PA (ORCH-) ORCHID BIOCOMPUTER INC.
Query Match 10.0%; Score 242; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 621
ID AAY31903 standard; protein; 309 AA.
DE Human uncoupling protein 2.
PN W09948905-A1.
PD 30-SEP-1999.
PA (MUSC-) MUSC FOUND RES DEV.

Query Match 10.0%; Score 242; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 622
ID AAY44292 standard; protein; 309 AA.
DE Human uncoupling protein-2.
PN W0953953-A2.
PD 28-OCT-1999.
PA (UYVE-) UNIV VERMONT.
Query Match 10.0%; Score 242; DB 3; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 623
ID AAY45002 standard; protein; 309 AA.
DE Tularex human uncoupling protein-2.
PN W020006087-A2.
PD 10-FEB-2000.
PA (TULA-) TULARIK INC.
Query Match 10.0%; Score 242; DB 3; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 624
ID AAY44252 standard; protein; 309 AA.
DE Human mitochondrial anion carrier, uncoupling protein-2.
PN W09964458-A1.
PD 16-DEC-1999.
PA (UYBO-) UNIV BOSTON.
Query Match 10.0%; Score 242; DB 3; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 625
ID AAY97998 standard; protein; 309 AA.
DE Human uncoupling protein C5, SEQ ID NO:51.
PN US6057109-A.
PD 02-MAY-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.0%; Score 242; DB 3; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 626
ID AAB27018 standard; protein; 309 AA.
DE Protein associated with body weight disorders, SEQ ID NO: 51.
PN US6121017-A.
PD 19-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.0%; Score 242; DB 3; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 627
ID AAY72342 standard; protein; 309 AA.
DE Human uncoupling protein, UCP-2.
PN W0200078941-A2.
PD 28-DEC-2000.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
Query Match 10.0%; Score 242; DB 4; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 628
ID ABO14802 standard; protein; 309 AA.
DE Human protein differentially expressed in obese/lean tissue C5.
PN US6518402-B1.
PD 11-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.0%; Score 242; DB 7; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 629
ID ADK18478 standard; protein; 309 AA.
DE Human NOVX protein #66.
PN W02003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 242; DB 7; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 630
ID ADP65162 standard; protein; 309 AA.
DE Human uncoupling protein 2.
PN W02003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.0%; Score 242; DB 7; Length 309;

Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 631
ID ADJ75632 standard; protein; 309 AA.
DE Marker gene related amino acid sequence SEQ ID NO:884.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 10.0%; Score 242; DB 8; Length 309;
Best Local Similarity 26.6%; Pred. No. 6.6e-14;
RESULT 632
ID AAU09077 standard; protein; 314 AA.
DE Human uncoupling protein, UCP-2.
PN W0200175131-A2.
PD 11-OCT-2001.
PA (UYTE-) UNIV TECHNOLOGY CORP.
Query Match 10.0%; Score 242; DB 4; Length 314;
Best Local Similarity 26.6%; Pred. No. 6.8e-14;
RESULT 633
ID ADN22668 standard; protein; 323 AA.
DE Bacterial polypeptide #5321.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 10.0%; Score 242; DB 8; Length 323;
Best Local Similarity 23.5%; Pred. No. 7.1e-14;
RESULT 634
ID AAG27857 standard; protein; 285 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32857.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.9%; Score 240.5; DB 3; Length 285;
Best Local Similarity 27.0%; Pred. No. 8.1e-14;
RESULT 635
ID ADJ33820 standard; protein; 421 AA.
DE Protein of the invention SEQ ID NO:797.
PN W0200187917-A1.
PD 22-NOV-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.9%; Score 240.5; DB 5; Length 421;
Best Local Similarity 23.5%; Pred. No. 1.5e-13;
RESULT 636
ID AAM23998 standard; protein; 299 AA.
DE Partial human C5 gene product.
PN US5702902-A.
PD 30-DEC-1997.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.9%; Score 239.5; DB 2; Length 299;
Best Local Similarity 26.6%; Pred. No. 1.1e-13;
RESULT 637
ID ABB92005 standard; protein; 844 AA.
DE Herbicidally active polypeptide SEQ ID NO 1216.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 9.9%; Score 239; DB 5; Length 844;
Best Local Similarity 19.9%; Pred. No. 5.8e-13;
RESULT 638
ID AAG20660 standard; protein; 249 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22937.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.8%; Score 238.5; DB 3; Length 249;
Best Local Similarity 28.5%; Pred. No. 1e-13;
RESULT 639
ID AAM50570 standard; protein; 351 AA.
DE Human mitochondrial carrier protein CGI-69.
PN W0200198355-A2.
PD 27-DEC-2001.
PA (GETH) GENENTECH INC.

PA (CURA-) CURAGEN CORP.
Query Match 9.8%; Score 238.5; DB 5; Length 351;
Best Local Similarity 22.9%; Pred. No. 1.7e-13;
RESULT 640
ID AAM81885 standard; protein; 351 AA.
DE Tumour-associated antigenic target (TAR) polypeptide PRO82743, SEQ:4848.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 238.5; DB 8; Length 351;
Best Local Similarity 22.9%; Pred. No. 1.7e-13;
RESULT 641
ID AAM85669 standard; protein; 309 AA.
DE Human UCP-2 (uncoupling protein).
PN W09845313-A1.
PD 15-OCT-1998.
PA (AMYL-) AMYLIN PHARM INC.
Query Match 9.8%; Score 238; DB 2; Length 309;
Best Local Similarity 26.6%; Pred. No. 1.6e-13;
RESULT 642
ID AAM81587 standard; protein; 312 AA.
DE Human uncoupling protein 3 (UCP3).
PN W09845438-A1.
PD 15-OCT-1998.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Query Match 9.8%; Score 238; DB 2; Length 312;
Best Local Similarity 26.2%; Pred. No. 1.6e-13;
RESULT 643
ID AAB58022 standard; protein; 1812 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 858.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.8%; Score 238; DB 4; Length 1812;
Best Local Similarity 22.5%; Pred. No. 2.3e-12;
RESULT 644
ID AAG39400 standard; protein; 249 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48744.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 9.8%; Score 237.5; DB 3; Length 249;
Best Local Similarity 28.5%; Pred. No. 1.3e-13;
RESULT 645
ID AAB59480 standard; protein; 323 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5232.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.8%; Score 237.5; DB 4; Length 323;
Best Local Similarity 25.7%; Pred. No. 1.9e-13;
RESULT 646
ID AAB50378 standard; protein; 351 AA.
DE Human uncoupling protein #1.
PN W0200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.8%; Score 237.5; DB 3; Length 351;
Best Local Similarity 23.2%; Pred. No. 2.1e-13;
RESULT 647
ID ADOS6898 standard; protein; 351 AA.
DE Human regulatory molecule HRM-19.
PN US2002058264-A1.
PD 16-MAY-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 9.8%; Score 237.5; DB 8; Length 351;
Best Local Similarity 23.2%; Pred. No. 2.1e-13;
RESULT 648
ID ADQ97536 standard; protein; 292 AA.
DE Mouse cancer associated sequence MP09-010, SEQ ID 513.
PN W02004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.8%; Score 237; DB 8; Length 292;

Best Local Similarity 25.8%; Pred. No. 1.8e-13;
RESULT 649
ID ADA05786 standard; protein; 290 AA.
DE Human NOV35b protein SEQ ID NO:146.
PN W02003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.8%; Score 236.5; DB 6; Length 290;
Best Local Similarity 26.4%; Pred. No. 2e-13;
RESULT 650
ID ADY70283 standard; protein; 409 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2089.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 9.8%; Score 236.5; DB 7; Length 409;
Best Local Similarity 28.5%; Pred. No. 3.3e-13;
RESULT 651
ID ADS2433 standard; protein; 422 AA.
DE Bacterial polypeptide #13366.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.8%; Score 236.5; DB 8; Length 422;
Best Local Similarity 29.2%; Pred. No. 3.5e-13;
RESULT 652
ID ABB43034 standard; peptide; 56 AA.
DE Peptide #10540 encoded by human foetal liver single exon probe.
PN W0200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 9.7%; Score 236; DB 4; Length 56;
Best Local Similarity 76.8%; Pred. No. 1.9e-14;
RESULT 653
ID AAM36864 standard; protein; 56 AA.
DE Peptide #10901 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 9.7%; Score 236; DB 4; Length 56;
Best Local Similarity 76.8%; Pred. No. 1.9e-14;
RESULT 654
ID AAM76757 standard; protein; 56 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37063.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 9.7%; Score 236; DB 4; Length 56;
Best Local Similarity 76.8%; Pred. No. 1.9e-14;
RESULT 655
ID AAM63939 standard; protein; 56 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36044.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 9.7%; Score 236; DB 4; Length 56;
Best Local Similarity 76.8%; Pred. No. 1.9e-14;
RESULT 656
ID ABG58440 standard; peptide; 56 AA.
DE Human liver peptide, SEQ ID NO 37088.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 9.7%; Score 236; DB 4; Length 56;
Best Local Similarity 76.8%; Pred. No. 1.9e-14;
RESULT 657
ID AAM83910 standard; protein; 215 AA.
DE Human diagnostic and therapeutic pproetin SEQ ID NO:4159.

PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.7%; Score 236; DB 8; Length 215;
RESULT 658
ID ABB83906 standard; protein; 215 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:4155.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.7%; Score 236; DB 8; Length 215;
Best Local Similarity 29.9%; Pred. No. 1.4e-13;
RESULT 659
ID AAM83379 standard; protein; 312 AA.
DE Human uncoupling protein UCP3L.
PN WO9850542-A1.
PD 12-NOV-1998.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
Query Match 9.7%; Score 236; DB 2; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 660
ID AAM8197 standard; protein; 312 AA.
DE Human uncoupling protein HNF6W60.
PN WO9839432-A1.
PD 11-SEP-1998.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 9.7%; Score 236; DB 2; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 661
ID AAM8567 standard; protein; 312 AA.
DE Human UCP-3 (uncoupling protein) .
PN WO9845313-A1.
PD 15-OCT-1998.
PA (AMTY-) AMTWIN PHARM INC.
Query Match 9.7%; Score 236; DB 2; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 662
ID AAM88279 standard; protein; 312 AA.
DE Human uncoupling protein 3 (UCP3) .
PN WO9852958-A1.
PD 26-NOV-1998.
PA (MERI) MERCK & CO INC.
Query Match 9.7%; Score 236; DB 2; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 663
ID AAY31904 standard; protein; 312 AA.
DE Human uncoupling protein 3.
PN WO9948905-A1.
PD 30-SEP-1999.
PA (MUSC-) MUSC FOUND RES DEV.
Query Match 9.7%; Score 236; DB 2; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 664
ID AAY54600 standard; protein; 312 AA.
DE Amino acid sequence of a human uncoupling protein designated HHFCW60.
PN WO200002577-A1.
PD 20-JAN-2000.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 9.7%; Score 236; DB 3; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 665
ID AAY44253 standard; protein; 312 AA.
DE Human mitochondrial anion carrier, uncoupling protein-3.
PN WO9964458-A1.
PD 16-DEC-1999.
PA (UYBO-) UNIV BOSTON.
Query Match 9.7%; Score 236; DB 3; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 666
ID AAB74296 standard; protein; 312 AA.
DE Human UCP3 protein.

PN WO200118232-A2.
PD 15-MAR-2001.
PA (GENA-) GENAISANCE PHARM INC.
PA (STEP/) STEPHENS J C.
Query Match 9.7%; Score 236; DB 4; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 667
ID AAE04298 standard; protein; 312 AA.
DE Human uncoupling protein-3 (UCP3) .
PN WO200143760-A2.
PD 21-JUN-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 9.7%; Score 236; DB 4; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 668
ID AAB68050 standard; protein; 312 AA.
DE Amino acid sequence of a human uncoupling protein 3 (UCP3) .
PN WO200124625-A1.
PD 12-APR-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 9.7%; Score 236; DB 4; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 669
ID AAB81610 standard; protein; 312 AA.
DE UCP3L protein sequence.
PN US2002065239-A1.
PD 30-MAY-2002.
PA (CAPL/) CAPLAN S L.
PA (BOET/) BOETTCHER B R.
PA (SLOS/) SLOSBERG E D.
PA (CONN/) CONNELLY S.
PA (KALE/) KALEKO M.
PA (DESA/) DESAI U J.
Query Match 9.7%; Score 236; DB 5; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 670
ID AAE19348 standard; protein; 312 AA.
DE Human mitochondrial uncoupling protein 3 (UCP3) .
PN WO200207754-A2.
PD 31-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 9.7%; Score 236; DB 5; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 671
ID ADE54391 standard; protein; 312 AA.
DE Human Protein P55916, SEQ ID NO 194.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 9.7%; Score 236; DB 7; Length 312;
Best Local Similarity 26.2%; Pred. No. 2.5e-13;
RESULT 672
ID ADX18476 standard; protein; 321 AA.
DE Human NOVX protein #65.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.7%; Score 236; DB 7; Length 321;
Best Local Similarity 25.7%; Pred. No. 2.6e-13;
RESULT 673
ID ADN19550 standard; protein; 335 AA.
DE Bacterial polypeptide #2203.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.7%; Score 236; DB 8; Length 335;
Best Local Similarity 24.6%; Pred. No. 2.8e-13;
RESULT 674

ID AAM81588 standard; protein: 403 AA.
DE Protein encoded by human UCP3 gene. reading frame 1.
PN W09845438-A1.
PD 15-OCT-1998.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Query Match 9.7%; Score 236; DB 2; Length 403;
Best Local Similarity 26.2%; Pred. No. 3.7e-13;
RESULT 675
ID AAO16964 standard; protein: 309 AA.
DE A thaliana mitochondrial carrier family protein encoded by AtACR1 gene.
PN W0200210394-A2.
PD 07-FEB-2002.
PA (FROM/) FROMMER W.
Query Match 9.7%; Score 235; DB 5; Length 309;
Best Local Similarity 26.1%; Pred. No. 3.1e-13;
RESULT 676
ID ADF75243 standard; protein: 309 AA.
DE Thale cress protein essential for plant growth and development SegID60.
PN W02003074653-A2.
PD 12-SEP-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 9.7%; Score 235; DB 7; Length 309;
Best Local Similarity 26.1%; Pred. No. 3.1e-13;
RESULT 677
ID ADH32310 standard; protein: 161 AA.
DE Novel yeast smorf564-encoded polypeptide, SEQ ID NO:768.
PN W0200268693-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.7%; Score 234.5; DB 5; Length 161;
Best Local Similarity 37.8%; Pred. No. 1.3e-13;
RESULT 678
ID ADN62948 standard; protein: 286 AA.
DE Human NOV35a.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILT/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (BLLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILT/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PEN/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEER M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 9.7%; Score 234.5; DB 8; Length 286;
Best Local Similarity 26.5%; Pred. No. 3e-13;
RESULT 679

ID ADN63240 standard; protein: 286 AA.
DE Human NOV35a variant.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILT/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (BLLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILT/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PEN/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEER M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 9.7%; Score 234.5; DB 8; Length 286;
Best Local Similarity 26.5%; Pred. No. 3e-13;
RESULT 680
ID ADN22925 standard; protein: 312 AA.
DE Bacterial polypeptide #5578.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.7%; Score 234.5; DB 8; Length 312;
Best Local Similarity 28.1%; Pred. No. 3.5e-13;
RESULT 681
ID ABB66897 standard; protein: 321 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27483.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.7%; Score 234.5; DB 4; Length 321;
Best Local Similarity 25.6%; Pred. No. 3.6e-13;
RESULT 682
ID AAR91282 standard; protein: 309 AA.
DE Body weight disorder-associated gene C5 product.
PN W09605861-A1.
PD 29-FEB-1996.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 9.7%; Score 234; DB 2; Length 309;
Best Local Similarity 26.3%; Pred. No. 3.8e-13;
RESULT 683
ID AAY05713 standard; protein: 447 AA.
DE Human adenine nucleotide translocator ANT5-related protein.
PN EP91341-A1.
PD 28-APR-1999.

PA (SMIK) SMITHKLINE BEECHAM LAB PHARM.
Query Match 9.7%; Score 234; DB 2; Length 447;
Best Local Similarity 28.8%; Pred. No. 6.6e-13;
RESULT 684
ID ADA05788 standard; protein; 270 AA.
DE Human NOV35c protein SEQ ID NO:148.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.6%; Score 233.5; DB 6; Length 270;
Best Local Similarity 26.5%; Pred. No. 3.5e-13;
RESULT 685
ID ADN62952 standard; protein; 270 AA.
DE Human NOV35C.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CAT/) CATTERTON E.
PA (JIMM/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PEN/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANCOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 9.6%; Score 233.5; DB 8; Length 270;
Best Local Similarity 26.5%; Pred. No. 3.5e-13;
RESULT 686
ID ADA05784 standard; protein; 286 AA.
DE Human NOV35a protein SEQ ID NO:144.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.6%; Score 233.5; DB 6; Length 286;
Best Local Similarity 26.5%; Pred. No. 3.8e-13;
RESULT 687
ID ADM03845 standard; protein; 289 AA.
DE Human protein of the invention SEQ ID NO:2530.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.6%; Score 233.5; DB 7; Length 289;
Best Local Similarity 27.1%; Pred. No. 3.8e-13;
RESULT 688
ID AAB50381 standard; protein; 323 AA.
DE Human uncoupling protein #4.
PN WO200061614-A2.
PD 19-OCT-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.6%; Score 233.5; DB 3; Length 323;
Best Local Similarity 25.2%; Pred. No. 4.5e-13;
RESULT 689
ID AAB94434 standard; protein; 323 AA.
DE Human protein sequence SEQ ID NO:15054.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 9.6%; Score 233.5; DB 4; Length 323;
Best Local Similarity 25.2%; Pred. No. 4.5e-13;
RESULT 690
ID AAB69215 standard; protein; 323 AA.
DE Human polypeptide SEQ ID NO 1262.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 9.6%; Score 233.5; DB 5; Length 323;
Best Local Similarity 25.2%; Pred. No. 4.5e-13;
RESULT 691
ID AAM50569 standard; protein; 359 AA.
DE Human mitochondrial carrier protein CGI-69L.
PN WO200198355-A2.
PD 27-DEC-2001.
PA (GETH/) GENENTECH INC.
PA (CURA-) CURAGEN CORP.
Query Match 9.6%; Score 233.5; DB 5; Length 359;
Best Local Similarity 22.6%; Pred. No. 5.3e-13;
RESULT 692
ID ADT66744 standard; protein; 359 AA.
DE Human CGI-69 protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF-) GRUNENTHAL GMBH.
Query Match 9.6%; Score 233.5; DB 8; Length 359;
Best Local Similarity 22.6%; Pred. No. 5.3e-13;
RESULT 693
ID AAG06601 standard; protein; 295 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3432.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.6%; Score 233; DB 3; Length 295;
Best Local Similarity 26.1%; Pred. No. 4.4e-13;
RESULT 694
ID AAG06600 standard; protein; 309 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3431.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.6%; Score 233; DB 3; Length 309;
Best Local Similarity 26.1%; Pred. No. 4.7e-13;
RESULT 695
ID AAB43372 standard; protein; 296 AA.
DE Human ORFX ORF3136 polypeptide sequence SEQ ID NO:6272.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 9.6%; Score 232.5; DB 3; Length 296;
Best Local Similarity 26.6%; Pred. No. 4.9e-13;
RESULT 696
ID AAB85025 standard; protein; 316 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:5274.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.6%; Score 232.5; DB 8; Length 316;
Best Local Similarity 25.9%; Pred. No. 5.4e-13;
RESULT 697
ID AAG23374 standard; protein; 266 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26657.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.6%; Score 232; DB 3; Length 266;
Best Local Similarity 25.7%; Pred. No. 4.7e-13;

RESULT 698
ID AAG40399 standard; protein; 266 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50121.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.6%; Score 232; DB 3; Length 266;
Pred. No. 4.7e-13;
RESULT 699
ID ADS44141 standard; protein; 329 AA.
DE Bacterial polypeptide #22571.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.6%; Score 232; DB 8; Length 329;
Pred. No. 6.4e-13;
RESULT 700
ID ADN99603 standard; protein; 342 AA.
DE Novel human protein sequence #419.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 9.6%; Score 232; DB 8; Length 342;
Pred. No. 6.8e-13;
RESULT 701
ID AAR91281 standard; protein; 299 AA.
DE Human body weight disorder-associated gene C5 product.
PN WO9605861-A1.
PD 29-FEB-1996.
PA (MILL-) MILLENITUM PHARM INC.
Query Match
Best Local Similarity 9.6%; Score 231.5; DB 2; Length 299;
Pred. No. 6.2e-13;
RESULT 702
ID ADJ66627 standard; protein; 213 AA.
DE Adenine nucleotide transporter protein for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 9.5%; Score 231; DB 8; Length 213;
Pred. No. 4.2e-13;
RESULT 703
ID ADN22828 standard; protein; 296 AA.
DE Bacterial polypeptide #5481.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.5%; Score 231; DB 8; Length 296;
Pred. No. 6.8e-13;
RESULT 704
ID AAM81595 standard; protein; 308 AA.
DE Mouse uncoupling protein 3. (UCP3).
PN WO9845438-A1.
PD 15-OCT-1998.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Query Match
Best Local Similarity 9.5%; Score 231; DB 2; Length 308;
Pred. No. 7.3e-13;
RESULT 705
ID AAM88280 standard; protein; 308 AA.
DE Mouse uncoupling protein 3 (UCP3).
PN WO9852958-A1.
PD 25-NOV-1998.
PA (MERK) MERCK & CO INC.
Query Match
Best Local Similarity 9.5%; Score 231; DB 2; Length 308;
Pred. No. 7.3e-13;
RESULT 706
ID AAY29835 standard; protein; 432 AA.

DE Mouse uncoupling protein 3 polypeptide #2.
PN US9592469-A.
PD 14-SEP-1999.
PA (TULA-) TULARIK INC.
Query Match
Best Local Similarity 9.5%; Score 231; DB 2; Length 432;
Pred. No. 1.2e-12;
RESULT 707
ID AAW85117 standard; protein; 432 AA.
DE A murine uncoupling protein designated mUCP3b.
PN US5846779-A.
PD 08-DEC-1998.
PA (TULA-) TULARIK INC.
Query Match
Best Local Similarity 9.5%; Score 231; DB 2; Length 432;
Pred. No. 1.2e-12;
RESULT 708
ID AAY77453 standard; protein; 432 AA.
DE Murine mitochondrial uncoupling protein isoform mUCP3b.
PN US6025469-A.
PD 15-FEB-2000.
PA (TULA-) TULARIK INC.
Query Match
Best Local Similarity 9.5%; Score 231; DB 3; Length 432;
Pred. No. 1.2e-12;
RESULT 709
ID AAE04730 standard; protein; 432 AA.
DE Mouse uncoupling protein 3b (mUCP3b) protein.
PN US6246561-B1.
PD 19-JUN-2001.
PA (TULA-) TULARIK INC.
Query Match
Best Local Similarity 9.5%; Score 231; DB 4; Length 432;
Pred. No. 1.2e-12;
RESULT 710
ID ADS23903 standard; protein; 358 AA.
DE Bacterial polypeptide #12936.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.5%; Score 230.5; DB 8; Length 358;
Pred. No. 1e-12;
RESULT 711
ID ADB85146 standard; protein; 301 AA.
DE Rat carnitine carrier protein SEQ ID NO:27.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match
Best Local Similarity 9.5%; Score 230; DB 7; Length 301;
Pred. No. 8.7e-13;
RESULT 712
ID AAM81596 standard; protein; 397 AA.
DE Protein encoded by mouse UCP3 gene reading frame 1.
PN WO9845438-A1.
PD 15-OCT-1998.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Query Match
Best Local Similarity 9.5%; Score 230; DB 2; Length 397;
Pred. No. 1.3e-12;
RESULT 713
ID ABB66966 standard; protein; 311 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27690.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 9.5%; Score 229.5; DB 4; Length 311;
Pred. No. 1e-12;
RESULT 714
ID AAB35982 standard; protein; 306 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5538.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 9.5%; Score 229; DB 4; Length 306;

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Best Local Similarity 25.5%; Pred. No. 1.1e-12;
RESULT 715
ID ADS43968 standard; protein; 307 AA.
DE Bacterial polypeptide #22398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.5%; Score 229; DB 8; Length 307;
Best Local Similarity 25.9%; Pred. No. 1.1e-12;
RESULT 716
ID ABP34498 standard; protein; 109 AA.
DE Human OREF471 protein, SEQ ID NO:6942.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 228.5; DB 5; Length 109;
Best Local Similarity 48.0%; Pred. No. 2.6e-13;
RESULT 717
ID ADM19898 standard; protein; 169 AA.
DE Protein encoded by novel human channel/transporter gene #216.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.4%; Score 228.5; DB 4; Length 169;
Best Local Similarity 34.0%; Pred. No. 5.1e-13;
RESULT 718
ID AMM20138 standard; protein; 198 AA.
DE Protein encoded by novel human channel/transporter gene #216 clone 2.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.4%; Score 228.5; DB 4; Length 198;
Best Local Similarity 34.0%; Pred. No. 6.5e-13;
RESULT 719
ID ADN62950 standard; protein; 290 AA.
DE Human NOV35d.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUIJ/) JU J.
PA (LILJ/) LI L.
PA (GUOX/) GUO X.
PA (PATY/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORIT/) ORT F.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATY/) CATTERTON E.
PA (JIWJ/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C B A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
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PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 9.4%; Score 228.5; DB 8; Length 290;
Best Local Similarity 26.1%; Pred. No. 1.1e-12;
RESULT 720
ID AAY29634 standard; protein; 308 AA.
DE Mouse uncoupling protein 3 polypeptide #1.
PN US9592469-A.
PD 14-SEP-1999.
PA (TULA-) TULARIK INC.
Query Match 9.4%; Score 228; DB 2; Length 308;
Best Local Similarity 27.1%; Pred. No. 1.4e-12;
RESULT 721
ID AAW85116 standard; protein; 308 AA.
DE A murine uncoupling protein designated mUCP3a.
PN US5846779-A.
PD 08-DEC-1998.
PA (TULA-) TULARIK INC.
Query Match 9.4%; Score 228; DB 2; Length 308;
Best Local Similarity 27.1%; Pred. No. 1.4e-12;
RESULT 722
ID AAY77452 standard; protein; 308 AA.
DE Marine mitochondrial uncoupling protein isoform mUCP3a.
PN US6025469-A.
PD 15-FEB-2000.
PA (TULA-) TULARIK INC.
Query Match 9.4%; Score 228; DB 3; Length 308;
Best Local Similarity 27.1%; Pred. No. 1.4e-12;
RESULT 723
ID AAB04729 standard; protein; 308 AA.
DE Mouse uncoupling protein 3a (mUCP3a) protein.
PN US6248561-B1.
PD 19-JUN-2001.
PA (TULA-) TULARIK INC.
Query Match 9.4%; Score 228; DB 4; Length 308;
Best Local Similarity 27.1%; Pred. No. 1.4e-12;
RESULT 724
ID ABO07114 standard; protein; 299 AA.
DE Novel human protein NOV3a.
PN WO200298900-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 227.5; DB 6; Length 299;
Best Local Similarity 25.6%; Pred. No. 1.5e-12;
RESULT 725
ID ADN23035 standard; protein; 328 AA.
DE Bacterial polypeptide #5668.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.4%; Score 227; DB 8; Length 328;
Best Local Similarity 23.4%; Pred. No. 1.9e-12;
RESULT 726
ID ADN62954 standard; protein; 254 AA.
DE Human NOV35d.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUIJ/) JU J.
PA (LILJ/) LI L.
PA (GUOX/) GUO X.
PA (PATY/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
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PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENNA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEER M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match
Best Local Similarity 9.3%; Score 226.5; DB 8; Length 254;
RESULT 727
ID AAW85668 standard; protein; 307 AA.
DE Human UCP-1 (uncoupling protein).
PN W09845313-A1.
PD 15-OCT-1998.
PA (AMYL-) AMYLIN PHARM INC.
Query Match
Best Local Similarity 9.3%; Score 226.5; DB 2; Length 307;
RESULT 728
ID ADN23515 standard; protein; 340 AA.
DE Bacterial polypeptide #6168.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.3%; Score 226; DB 8; Length 340;
RESULT 729
ID ADN23516 standard; protein; 340 AA.
DE Bacterial polypeptide #6169.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.3%; Score 226; DB 8; Length 340;
RESULT 730
ID ADC39083 standard; protein; 293 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 22.
PN W02003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.3%; Score 225.5; DB 7; Length 293;
RESULT 731
ID AAY44291 standard; protein; 307 AA.
DE Human uncoupling protein-1.
PN W0953953-A2.
PD 28-OCT-1999.
PA (UYVE-) UNIV VERMONT.
Query Match
Best Local Similarity 9.3%; Score 225.5; DB 3; Length 307;
RESULT 732

RESULT 732
ID AAY44251 standard; protein; 307 AA.
DE Human mitochondrial anion carrier, uncoupling protein-1.
PN W09964458-A1.
PD 16-DEC-1999.
PA (UYBO-) UNIV BOSTON.
Query Match
Best Local Similarity 9.3%; Score 225.5; DB 3; Length 307;
RESULT 733
ID AAU09076 standard; protein; 307 AA.
DE Human uncoupling protein, UCP-1.
PN W0200175131-A2.
PD 11-OCT-2001.
PA (UYTE-) UNIV TECHNOLOGY CORP.
Query Match
Best Local Similarity 9.3%; Score 225.5; DB 4; Length 307;
RESULT 734
ID AAY72341 standard; protein; 307 AA.
DE Human uncoupling protein, UCP-1.
PN W0200078941-A2.
PD 28-DEC-2000.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
Query Match
Best Local Similarity 9.3%; Score 225.5; DB 4; Length 307;
RESULT 735
ID AAY31932 standard; protein; 180 AA.
DE Soybean Dittle-1 partial polypeptide.
PN W09949047-A2.
PD 30-SEP-1999.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 9.3%; Score 225; DB 2; Length 180;
RESULT 736
ID AAO16963 standard; protein; 296 AA.
DE A thaliana mitochondrial carrier family protein encoded by AtARG11 gene.
PN W0200210394-A2.
PD 07-FEB-2002.
PA (FROM/) FROMMER W.
Query Match
Best Local Similarity 9.3%; Score 224.5; DB 5; Length 296;
RESULT 737
ID ABB62682 standard; protein; 357 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3735.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 9.2%; Score 224; DB 8; Length 357;
RESULT 738
ID ABB62682 standard; protein; 317 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14838.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 9.2%; Score 223.5; DB 4; Length 317;
RESULT 739
ID AAB38268 standard; protein; 379 AA.
DE Rice grain quality and nutritional composition protein, BT1.
PN W02003048319-A2.
PD 12-JUN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 9.2%; Score 223.5; DB 6; Length 379;
RESULT 740
ID ADC39190 standard; protein; 220 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 132.
PN W02003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.2%; Score 223; DB 7; Length 220;
RESULT 741

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ID AAG05380 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1766.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.2%; Score 223; DB 3; Length 305;
Pred. No. 4.1e-12;
RESULT 742
ID AAG48337 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61029.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.2%; Score 223; DB 3; Length 305;
Pred. No. 4.1e-12;
RESULT 743
ID AAG37832 standard; protein; 211 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46583.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 3; Length 211;
Pred. No. 2.6e-12;
RESULT 744
ID AAG39528 standard; protein; 211 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48921.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 3; Length 211;
Pred. No. 2.6e-12;
RESULT 745
ID AAG37831 standard; protein; 232 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46582.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 3; Length 232;
Pred. No. 3e-12;
RESULT 746
ID AAG39527 standard; protein; 232 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48920.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 3; Length 232;
Pred. No. 3e-12;
RESULT 747
ID AAG23666 standard; protein; 241 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27058.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 3; Length 241;
Pred. No. 3.2e-12;
RESULT 748
ID AAB50380 standard; protein; 301 AA.
DE Human uncoupling protein #3.
PN W0200061614-A2.
PD 19-OCT-2000.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 3; Length 301;
Pred. No. 4.5e-12;
RESULT 749
ID AAE16767 standard; protein; 301 AA.
DE Human transporter and ion channel-4 (TRICH-4) protein.
PN W0200192304-A2.
PD 06-DEC-2001.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 5; Length 301;
Pred. No. 4.5e-12;
RESULT 750
ID ADS44323 standard; protein; 379 AA.
DE Bacterial polypeptide #22753.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.1%; Score 221.5; DB 8; Length 301;
Pred. No. 6.2e-12;
RESULT 751
ID ADS44324 standard; protein; 379 AA.
DE Bacterial polypeptide #22754.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.2%; Score 222.5; DB 8; Length 379;
Pred. No. 6.3e-12;
RESULT 752
ID ABB66414 standard; protein; 356 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 26034.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 9.2%; Score 222; DB 4; Length 356;
Pred. No. 6.4e-12;
RESULT 753
ID ABB71335 standard; protein; 356 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 40797.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 9.2%; Score 222; DB 4; Length 356;
Pred. No. 6.4e-12;
RESULT 754
ID AAB50385 standard; protein; 183 AA.
DE Human uncoupling protein #8.
PN W0200061614-A2.
PD 19-OCT-2000.
Query Match
Best Local Similarity 9.1%; Score 221.5; DB 3; Length 183;
Pred. No. 2.6e-12;
RESULT 755
ID AAM39504 standard; protein; 183 AA.
DE Human polypeptide SEQ ID NO: 2649.
PN W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 9.1%; Score 221.5; DB 4; Length 183;
Pred. No. 2.6e-12;
RESULT 756
ID AAG13088 standard; protein; 211 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12450.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.1%; Score 221.5; DB 3; Length 211;
Pred. No. 3.3e-12;
RESULT 757
ID AAG13087 standard; protein; 232 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12449.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.1%; Score 221.5; DB 3; Length 232;
Pred. No. 3.8e-12;
RESULT 758
ID ADN21487 standard; protein; 301 AA.
DE Bacterial polypeptide #4140.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.1%; Score 221; DB 8; Length 301;
Pred. No. 6.2e-12;
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RESULT 759
ID AAB56315 standard; protein: 305 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1737.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 9.1%; Score 221; DB 4; Length 305;
Pred. No. 6.3e-12;
RESULT 760
ID AAG19643 standard; protein: 313 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21522.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.1%; Score 221; DB 3; Length 313;
Pred. No. 6.6e-12;
RESULT 761
ID AAG50517 standard; protein: 313 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64029.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 9.1%; Score 221; DB 3; Length 313;
Pred. No. 6.6e-12;
RESULT 762
ID ADN19242 standard; protein: 368 AA.
DE Bacterial polypeptide #1895.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.1%; Score 221; DB 8; Length 368;
Pred. No. 8.4e-12;
RESULT 763
ID AAE21183 standard; protein: 301 AA.
DE Human TRICH-27 protein.
PN W0200213340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 9.1%; Score 220.5; DB 5; Length 301;
Pred. No. 6.9e-12;
RESULT 764
ID AAB4783 standard; protein: 365 AA.
DE Human ORFX ORF2547 polypeptide sequence SEQ ID NO:5094.
PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.1%; Score 220.5; DB 3; Length 365;
Pred. No. 9.3e-12;
RESULT 765
ID AAR71458 standard; protein: 306 AA.
DE Human mitochondrial uncoupling protein 'thermogenin'.
PN W09506411-A1.
PD 09-MAR-1995.
PA (LIPO-) LIPOCYTE INC.
Query Match
Best Local Similarity 9.1%; Score 220; DB 2; Length 306;
Pred. No. 7.9e-12;
RESULT 766
ID ADA05790 standard; protein: 254 AA.
DE Human NOV35d protein SEQ ID NO:150.
PN W02003039424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 6; Length 254;
Pred. No. 6.7e-12;
RESULT 767
ID ABR52768 standard; protein: 311 AA.
DE Protein sequence #SEQ ID 401.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZONE AG.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 6; Length 311;

Best Local Similarity 27.1%; Pred. No. 9.1e-12;
RESULT 768
ID ADK62106 standard; protein: 311 AA.
DE Disease treating protein complex-derived protein #179.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZONE AG.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 7; Length 311;
Pred. No. 9.1e-12;
RESULT 769
ID ADS43766 standard; protein: 311 AA.
DE Bacterial polypeptide #22196.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 8; Length 311;
Pred. No. 9.1e-12;
RESULT 770
ID AAY81497 standard; protein: 323 AA.
DE Human uncoupling protein UCP4.
PN W0200017353-A1.
PD 30-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 3; Length 323;
Pred. No. 9.6e-12;
RESULT 771
ID AAY99457 standard; protein: 323 AA.
DE Human UCP4 amino acid sequence SEQ ID NO:406.
PN W020012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 3; Length 323;
Pred. No. 9.6e-12;
RESULT 772
ID AAB66206 standard; protein: 323 AA.
DE Protein of the invention #118.
PN W0200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 4; Length 323;
Pred. No. 9.6e-12;
RESULT 773
ID AAB87588 standard; protein: 323 AA.
DE Human PRO1566.
PN W0200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 4; Length 323;
Pred. No. 9.6e-12;
RESULT 774
ID ABG95913 standard; protein: 323 AA.
DE Human secreted/transmembrane protein PRO1566.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 5; Length 323;
Pred. No. 9.6e-12;
RESULT 775
ID ABU90938 standard; protein: 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.1%; Score 219.5; DB 6; Length 323;
Pred. No. 9.6e-12;
RESULT 776
ID ABO33997 standard; protein: 323 AA.
DE Human secreted/transmembrane protein PRO1566.
PN US2003009013-A1.

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PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 777
ID ABU72014 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 778
ID ABU71568 standard; protein; 323 AA.
DE Human secreted polypeptide PRO1566.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 779
ID ABU72349 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 780
ID ABU91022 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 781
ID ABO27343 standard; protein; 323 AA.
DE Human secreted/transmembrane polypeptide PRO1566.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 782
ID ABU92538 standard; protein; 323 AA.
DE Human secreted/transmembrane protein PRO1566.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 783
ID ABU81208 standard; protein; 323 AA.
DE Human secreted polypeptide PRO1566.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 784
ID ABO53322 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 785
ID ABU98325 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 786
ID ABU89330 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 787
ID ABU82537 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 788
ID ABU96501 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 789
ID ABU72171 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 790
ID ADB17183 standard; protein; 323 AA.
DE Human transmembrane PRO polypeptide (SeqID 126) .
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 791
ID ABO44301 standard; protein; 323 AA.
DE Human secreted/transmembrane polypeptide PRO 1566.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 792
ID ABO33699 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein UCP4.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 793
ID ADA19988 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 794
ID ADB17371 standard; protein; 323 AA.
DE Human transmembrane PRO polypeptide (SeqID 126) .
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match          9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 795
ID ADA20160 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 796
ID ABO34229 standard; protein; 323 AA.
DE Human secreted/transmembrane polypeptide PRO 1566.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 797
ID ADA00457 standard; protein; 323 AA.
DE Human secreted/transmembrane polypeptide PRO 1566.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 6; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 798
ID ABO44552 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 799
ID ABO33576 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein UCP4.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 800
ID ADB8569 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 801
ID ADB68378 standard; protein; 323 AA.
DE Human PRO1566 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 802
ID ADB68185 standard; protein; 323 AA.
DE Human PRO1566 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 803
ID ADB91002 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 804
ID ADC07082 standard; protein; 323 AA.
DE Human PRO1566 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 805
ID ADC18275 standard; protein; 323 AA.
DE Human PRO polypeptide #118.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 806
ID ADC17261 standard; protein; 323 AA.
DE Mammalian PRO polypeptide (SeqID 126).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 807
ID ADC14959 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 808
ID ADC52454 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 809
ID ADD70921 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 810
ID ADD3998 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 811
ID ADD7044 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 812
ID ADD36130 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
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RESULT 813
ID ADF38565 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 814
ID ADF39521 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 815
ID ADF39044 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 816
ID ADF40475 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 817
ID ADE50696 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 818
ID ADE20308 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 819
ID ADE50219 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 820
ID ADE21777 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 821
ID ADF30202 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 822

ID ADF56095 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 823
ID ADG01131 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 824
ID ADG06684 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 825
ID ADF95305 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 826
ID ADH24158 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 827
ID ADH34184 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 828
ID ADH30017 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 829
ID ADH23988 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 830
ID ADG85392 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 831
ID ADH24668 standard; protein; 323 AA.

DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 832
ID ADH37524 standard; protein; 323 AA.
DE Human secreted and transmembrane protein PRO1566.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 833
ID ADH02113 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 834
ID ADH37694 standard; protein; 323 AA.
DE Human secreted and transmembrane protein PRO1566.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 835
ID ADG85732 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 836
ID ADH24328 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 837
ID ADH38622 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 838
ID ADG83743 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 839
ID ADH23551 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 840
ID ADH27667 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 841
ID ADH37864 standard; protein; 323 AA.
DE Human secreted and transmembrane protein PRO1566.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 842
ID ADH38041 standard; protein; 323 AA.
DE Human secreted and transmembrane protein PRO1566.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 843
ID ADH57461 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 844
ID ADH53603 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 845
ID ADH53773 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 846
ID ADH52109 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 847
ID ADH49964 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 848
ID ADI25474 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 849
ID ADH90267 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181698-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 850
ID ADI25644 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 851
ID ADH97818 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 852
ID ADH99599 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 853
ID ADI03666 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 854
ID ADI12023 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 855
ID ADH90097 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 856
ID ADH98498 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 857
ID ADI11173 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 858
ID ADI11683 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 859
ID ADH93328 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 860
ID ADH98668 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 861
ID ADH98158 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 862
ID ADI05146 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 863
ID ADI03496 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 864
ID ADI04891 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 865
ID ADH78345 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 866
ID ADI19689 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 867
ID ADH90437 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 868
ID AD103156 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 869
ID ADH78005 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 870
ID ADH97988 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 871
ID AD101373 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 872
ID AD102068 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 873
ID AD103326 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 874
ID AD11513 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 875
ID AD102415 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 876
ID AD11853 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 877
ID AD105490 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 878
ID ADH79562 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 879
ID AD119519 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 880
ID AD105320 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 881
ID ADH79732 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 882
ID AD101558 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 883
ID AD101728 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 884
ID AD101898 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 885
ID ADH79902 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
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RESULT 886
ID ADI04720 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 887
ID ADI02856 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 888
ID ADH78175 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 889
ID ADI2814 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 890
ID ADI25984 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 891
ID ADK65496 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 892
ID ADH98838 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 893
ID ADH80079 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 894
ID ADL93809 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 7; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 895

ID ADC52264 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 896
ID ADE96779 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 897
ID ADP26090 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 898
ID ADP24989 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 899
ID ADF29725 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 900
ID ADE97256 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 901
ID ADH06696 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 902
ID ADH06526 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 903
ID ADG68947 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 904
ID ADH27837 standard; protein; 323 AA.

DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 905
ID ADH25178 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 906
ID ADH33810 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 907
ID ADH03294 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 908
ID ADH02453 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 909
ID ADH08060 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 910
ID ADG69457 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 911
ID ADH32977 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 912
ID ADH04248 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 913
ID ADH03771 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2003180916-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 914
ID ADG84018 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 915
ID ADG85562 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 916
ID ADH06356 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 917
ID ADH30186 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 918
ID ADH24498 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 919
ID ADG69627 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 920
ID ADH07890 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 921
ID ADG85902 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 922
ID ADH39448 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180916-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 923
ID ADH33640 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 924
ID ADH33980 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 925
ID ADH01190 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 926
ID ADG69797 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 927
ID ADH02283 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 928
ID ADG63287 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 929
ID ADG86072 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 930
ID ADH25008 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 931
ID ADH33625 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180915-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 932
ID ADH02623 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 933
ID ADG69117 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 934
ID ADH07720 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 935
ID ADG86242 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 936
ID ADH24838 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 937
ID ADH25886 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 938
ID ADH38452 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 939
ID ADH57291 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 940
ID ADH52278 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 941
ID ADH04725 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 942
ID ADH49644 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 943
ID ADH90607 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 944
ID ADI11343 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 945
ID ADH99008 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 946
ID ADI02238 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 947
ID ADH61726 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 948
ID ADH90777 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 949
ID ADM80982 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 950
ID ADH9822 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 951
ID ADH78981 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 952
ID ADH99215 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 953
ID ADH99385 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 954
ID ADJ99003 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 955
ID ADH79150 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 956
ID ADK01011 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 957
ID ADK14532 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO1566.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 958
ID ADM80981 standard; protein; 323 AA.
DE Human PRO polypeptide #63.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match          9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
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RESULT 959
ID ADL94925 standard; protein; 323 AA.
DE Human secreted/transmembrane protein UCP4.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 219.5; DB 8; Length 323;
Best Local Similarity 24.3%; Pred. No. 9.6e-12;
RESULT 960
ID AM39719 standard; protein; 268 AA.
DE Human polypeptide SEQ ID NO 2864.
PN W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.0%; Score 218.5; DB 4; Length 268;
Best Local Similarity 26.8%; Pred. No. 9e-12;
RESULT 961
ID ADN21453 standard; protein; 358 AA.
DE Bacterial polypeptide #4106.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.0%; Score 218.5; DB 8; Length 358;
Best Local Similarity 24.9%; Pred. No. 1.4e-11;
RESULT 962
ID AAG41403 standard; protein; 306 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51509.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 9.0%; Score 218; DB 3; Length 306;
Best Local Similarity 26.0%; Pred. No. 1.2e-11;
RESULT 963
ID ADN23385 standard; protein; 309 AA.
DE Bacterial polypeptide #6038.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.0%; Score 218; DB 8; Length 309;
Best Local Similarity 26.4%; Pred. No. 1.2e-11;
RESULT 964
ID ABB61381 standard; protein; 306 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10935.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.0%; Score 217.5; DB 4; Length 306;
Best Local Similarity 25.2%; Pred. No. 1.4e-11;
RESULT 965
ID ABB93306 standard; protein; 330 AA.
DE Herbicidally active polypeptide SEQ ID NO 2517.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 9.0%; Score 217.5; DB 5; Length 330;
Best Local Similarity 27.0%; Pred. No. 1.5e-11;
RESULT 966
ID ABO55248 standard; protein; 52 AA.
DE Human genome derived single exon protein #1482.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 9.0%; Score 217; DB 8; Length 52;
Best Local Similarity 82.0%; Pred. No. 1.1e-12;

RESULT 967
ID AAG07171 standard; protein; 289 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4222.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (PEKE) PE CORP NY.
Query Match 8.9%; Score 216.5; DB 3; Length 289;
Best Local Similarity 24.9%; Pred. No. 1.6e-11;
RESULT 968
ID AAG07170 standard; protein; 296 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4221.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.9%; Score 216.5; DB 3; Length 296;
Best Local Similarity 24.9%; Pred. No. 1.6e-11;
RESULT 969
ID ABP74106 standard; protein; 222 AA.
DE Human TRICH SEQ ID NO 11.
PN W0200246415-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.9%; Score 216; DB 5; Length 222;
Best Local Similarity 30.8%; Pred. No. 1.2e-11;
RESULT 970
ID ABG61536 standard; protein; 315 AA.
DE Human transporter and ion channel, TRICH6, Incyte ID 8128531CD1.
PN W0200240541-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.9%; Score 215.5; DB 5; Length 315;
Best Local Similarity 25.0%; Pred. No. 2.2e-11;
RESULT 971
ID ABG61537 standard; protein; 760 AA.
DE Human transporter and ion channel, TRICH7, Incyte ID 7476757CD1.
PN W0200240541-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.9%; Score 215.5; DB 5; Length 760;
Best Local Similarity 25.0%; Pred. No. 8.3e-11;
RESULT 972
ID ABB62409 standard; protein; 340 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14019.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.9%; Score 214.5; DB 4; Length 340;
Best Local Similarity 28.5%; Pred. No. 3.1e-11;
RESULT 973
ID AAG29875 standard; protein; 208 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35618.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.8%; Score 214; DB 3; Length 208;
Best Local Similarity 31.7%; Pred. No. 1.6e-11;
RESULT 974
ID AAG49737 standard; protein; 208 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62951.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.8%; Score 214; DB 3; Length 208;
Best Local Similarity 31.7%; Pred. No. 1.6e-11;
RESULT 975
ID AAG50519 standard; protein; 237 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64031.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.8%; Score 214; DB 3; Length 237;
Best Local Similarity 26.9%; Pred. No. 2e-11;
RESULT 976
ID AAG50518 standard; protein; 284 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64030.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.8%; Score 214; DB 3; Length 284;

Best Local Similarity 26.9%; Pred. No. 2.6e-11;
RESULT 977
ID AAG49736 standard; protein; 313 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62950.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 31.7%; Pred. No. 3e-11;
RESULT 978
ID AAG29874 standard; protein; 313 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35617.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 31.7%; Pred. No. 3e-11;
RESULT 979
ID AAG49735 standard; protein; 341 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62949.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 31.7%; Pred. No. 3.5e-11;
RESULT 980
ID AAG29873 standard; protein; 342 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35616.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 31.7%; Pred. No. 3.5e-11;
RESULT 981
ID AAM3937 standard; protein; 254 AA.
DE Human polypeptide SEQ ID NO 2082.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 26.4%; Pred. No. 2.5e-11;
RESULT 982
ID ABG75060 standard; protein; 314 AA.
DE Human solute carrier family 25 member 11 protein.
PN WO2003075945-A2.
PD 18-SEP-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match
Best Local Similarity 26.4%; Pred. No. 3.8e-11;
RESULT 983
ID ADI63106 standard; protein; 314 AA.
DE Human apoptosis-associated protein SEQ ID 549.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match
Best Local Similarity 26.4%; Pred. No. 3.8e-11;
RESULT 984
ID ADJ68692 standard; protein; 314 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID498.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 26.4%; Pred. No. 3.8e-11;
RESULT 985
ID ADJ71209 standard; protein; 314 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID3015.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 26.4%; Pred. No. 3.8e-11;
RESULT 986
ID ADJ70398 standard; protein; 314 AA.

DE Human heat mitochondrial protein as a therapeutic target SeqID2204.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 26.4%; Pred. No. 3.8e-11;
RESULT 987
ID ADG89940 standard; protein; 314 AA.
DE Antagonist of cell cycle progression polypeptide #185.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match
Best Local Similarity 26.4%; Pred. No. 3.8e-11;
RESULT 988
ID AAU29748 standard; protein; 677 AA.
DE Novel human secreted protein #239.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 26.7%; Pred. No. 1.3e-10;
RESULT 989
ID ABB40571 standard; peptide; 59 AA.
DE Peptide #8077 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 71.2%; Pred. No. 3.8e-12;
RESULT 990
ID AAM74219 standard; protein; 59 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34525.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 71.2%; Pred. No. 3.8e-12;
RESULT 991
ID AAM61429 standard; protein; 59 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33534.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 71.2%; Pred. No. 3.8e-12;
RESULT 992
ID ABG56022 standard; peptide; 59 AA.
DE Human liver peptide, SEQ ID No 34670.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 71.2%; Pred. No. 3.8e-12;
RESULT 993
ID AAB42980 standard; protein; 272 AA.
DE Human ORFX ORF2744 polypeptide sequence SEQ ID NO: 5488.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 25.3%; Pred. No. 3.8e-11;
RESULT 994
ID ABR41730 standard; protein; 272 AA.
DE Human DITP organelle-associated protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 25.3%; Pred. No. 3.8e-11;
RESULT 995
ID ABB5928 standard; protein; 299 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 6576.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.7%; Score 212; DB 4; Length 299;
Best Local Similarity 24.0%; Pred. No. 4.4e-11;
RESULT 996
ID ADC1156 standard; protein; 299 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1238.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 212; DB 7; Length 299;
Best Local Similarity 27.9%; Pred. No. 4.4e-11;
RESULT 997
ID ABB57921 standard; protein; 301 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 555.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.7%; Score 212; DB 4; Length 301;
Best Local Similarity 24.8%; Pred. No. 4.4e-11;
RESULT 998
ID ADQ8738 standard; protein; 301 AA.
DE Antagonist of cell cycle progression polypeptide #84.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 8.7%; Score 212; DB 8; Length 301;
Best Local Similarity 24.8%; Pred. No. 4.4e-11;
RESULT 999
ID ADS43573 standard; protein; 366 AA.
DE Bacterial polypeptide #22003.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOT/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.7%; Score 212; DB 8; Length 366;
Best Local Similarity 26.2%; Pred. No. 5.9e-11;
RESULT 1000
ID ADS24188 standard; protein; 176 AA.
DE Bacterial polypeptide #13221.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOT/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.7%; Score 211.5; DB 8; Length 176;
Best Local Similarity 36.4%; Pred. No. 2.2e-11;
RESULT 1001
ID ABB69108 standard; protein; 413 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34116.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.7%; Score 211.5; DB 4; Length 413;
Best Local Similarity 21.9%; Pred. No. 7.9e-11;
RESULT 1002
ID ADM04480 standard; protein; 216 AA.
DE Human protein of the invention SEQ ID NO:3165.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.7%; Score 211; DB 7; Length 216;
Best Local Similarity 32.3%; Pred. No. 3.3e-11;
RESULT 1003
ID ADJ68735 standard; protein; 301 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID541.

PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.7%; Score 211; DB 7; Length 301;
Best Local Similarity 23.6%; Pred. No. 5.5e-11;
RESULT 1004
ID ADJ68736 standard; protein; 301 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID542.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.7%; Score 211; DB 7; Length 301;
Best Local Similarity 23.6%; Pred. No. 5.5e-11;
RESULT 1005
ID AAM79434 standard; protein; 318 AA.
DE Human protein SEQ ID NO 3080.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 211; DB 4; Length 318;
Best Local Similarity 23.6%; Pred. No. 6e-11;
RESULT 1006
ID AAM78450 standard; protein; 318 AA.
DE Human protein SEQ ID NO 1112.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 211; DB 4; Length 318;
Best Local Similarity 23.6%; Pred. No. 6e-11;
RESULT 1007
ID AAB50393 standard; protein; 320 AA.
DE Human uncoupling protein #16.
PN WO200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.7%; Score 210.5; DB 3; Length 320;
Best Local Similarity 27.4%; Pred. No. 6.7e-11;
RESULT 1008
ID ABM74194 standard; protein; 362 AA.
DE DNA clone originating in barley containing SNP sequence #604.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 8.7%; Score 210.5; DB 7; Length 362;
Best Local Similarity 23.2%; Pred. No. 8.1e-11;
RESULT 1009
ID ABG00985 standard; protein; 2234 AA.
DE Novel human diagnostic protein #976.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 210.5; DB 4; Length 2234;
Best Local Similarity 31.5%; Pred. No. 1.2e-09;
RESULT 1010
ID AAG19645 standard; protein; 237 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21524.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 8.7%; Score 210; DB 3; Length 237;
Best Local Similarity 26.4%; Pred. No. 4.8e-11;
RESULT 1011
ID AAG19644 standard; protein; 284 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21523.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 8.7%; Score 210; DB 3; Length 284;
Best Local Similarity 26.4%; Pred. No. 6.3e-11;
RESULT 1012
ID ABB66905 standard; protein; 302 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27507.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.7%; Score 210; DB 4; Length 302;
Best Local Similarity 24.7%; Pred. No. 6.9e-11;
RESULT 1013
ID ABB62849 standard; protein; 307 AA.
DE Human polypeptide SEQ ID NO 286.
PN W0200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 8.7%; Score 210; DB 5; Length 307;
Best Local Similarity 24.7%; Pred. No. 7.1e-11;
RESULT 1014
ID ADD48797 standard; protein; 307 AA.
DE Human Protein NP_006349, SEQ ID NO 14507.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
Query Match 8.7%; Score 210; DB 7; Length 307;
Best Local Similarity 24.7%; Pred. No. 7.1e-11;
RESULT 1015
ID ADR89488 standard; protein; 307 AA.
DE Apoptosis-inducing protein, SEQ ID 12.
PN W02004078112-A2.
PD 16-SEP-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 8.7%; Score 210; DB 8; Length 307;
Best Local Similarity 24.7%; Pred. No. 7.1e-11;
RESULT 1016
ID ADN21301 standard; protein; 409 AA.
DE Bacterial polypeptide #3954.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.7%; Score 210; DB 8; Length 409;
Best Local Similarity 24.3%; Pred. No. 1.1e-10;
RESULT 1017
ID AAB50391 standard; protein; 301 AA.
DE Human uncoupling protein #14.
PN W0200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMA GENOME SCI INC.
Query Match 8.6%; Score 209.5; DB 3; Length 301;
Best Local Similarity 24.1%; Pred. No. 7.6e-11;
RESULT 1018
ID AAG46300 standard; protein; 318 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60979.
PN EF1033405-A2.
PD 06-SEP-2000.
Query Match 8.6%; Score 209.5; DB 3; Length 318;
Best Local Similarity 25.2%; Pred. No. 8.3e-11;
RESULT 1019
ID ADL61324 standard; protein; 301 AA.
DE Human solute carrier family 25 member 15 protein.
PN W02004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 8.6%; Score 208.5; DB 8; Length 301;
Best Local Similarity 24.1%; Pred. No. 9.5e-11;
RESULT 1020
ID ADE06348 standard; protein; 338 AA.
DE Novel protein (useful for identifying genetic disorders) #503.
PN W02003056152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.6%; Score 208.5; DB 7; Length 338;
Best Local Similarity 25.9%; Pred. No. 1.1e-10;
RESULT 1021

ID ADM20136 standard; protein; 170 AA.
DE Protein encoded by novel human channel/transporter gene #215 clone 2.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.6%; Score 208; DB 4; Length 170;
Best Local Similarity 34.5%; Pred. No. 4.5e-11;
RESULT 1022
ID ADM19897 standard; protein; 172 AA.
DE Protein encoded by novel human channel/transporter gene #215.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.6%; Score 208; DB 4; Length 172;
Best Local Similarity 34.5%; Pred. No. 4.6e-11;
RESULT 1023
ID ADM19899 standard; protein; 220 AA.
DE Protein encoded by novel human channel/transporter gene #217.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.6%; Score 208; DB 4; Length 220;
Best Local Similarity 26.5%; Pred. No. 6.6e-11;
RESULT 1024
ID AAM39948 standard; protein; 269 AA.
DE Human polypeptide SEQ ID NO 3093.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.6%; Score 208; DB 4; Length 269;
Best Local Similarity 26.4%; Pred. No. 9e-11;
RESULT 1025
ID ADJ33749 standard; protein; 335 AA.
DE Protein of the invention SEQ ID NO:726.
PN W0200187917-A1.
PD 22-NOV-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.6%; Score 208; DB 5; Length 335;
Best Local Similarity 22.7%; Pred. No. 1.2e-10;
RESULT 1026
ID AAM41734 standard; protein; 368 AA.
DE Human polypeptide SEQ ID NO 6665.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.6%; Score 208; DB 4; Length 368;
Best Local Similarity 26.4%; Pred. No. 1.4e-10;
RESULT 1027
ID AAB50384 standard; protein; 304 AA.
DE Human uncoupling protein #7.
PN W0200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.6%; Score 207.5; DB 3; Length 304;
Best Local Similarity 24.7%; Pred. No. 1.2e-10;
RESULT 1028
ID ADM48234 standard; protein; 358 AA.
DE Polypeptide sequence #284 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 8.6%; Score 207.5; DB 8; Length 358;
Best Local Similarity 21.9%; Pred. No. 1.5e-10;
RESULT 1029
ID AAM42051 standard; protein; 377 AA.
DE Human polypeptide SEQ ID NO 6982.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.6%; Score 207.5; DB 4; Length 377;
Best Local Similarity 24.7%; Pred. No. 1.7e-10;

RESULT 1030
ID ADN23431 standard; protein; 269 AA.
DE Bacterial polypeptide #6084.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.5%; Score 207; DB 8; Length 269;
Best Local Similarity 27.3%; Pred. No. 1.1e-10;
RESULT 1031
ID AAG89124 standard; protein; 274 AA.
DE Human secreted protein, SEQ ID NO: 244.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GSEST) GENSET.
Query Match 8.5%; Score 207; DB 4; Length 274;
Best Local Similarity 25.2%; Pred. No. 1.1e-10;
RESULT 1032
ID AAY90323 standard; protein; 293 AA.
DE Novel human protein sequence #2.
PN WO200047617-A1.
PD 17-AUG-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 8.5%; Score 207; DB 3; Length 293;
Best Local Similarity 27.9%; Pred. No. 1.3e-10;
RESULT 1033
ID ADN21044 standard; protein; 307 AA.
DE Bacterial polypeptide #3697.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.5%; Score 207; DB 8; Length 307;
Best Local Similarity 24.2%; Pred. No. 1.4e-10;
RESULT 1034
ID ADQ08618 standard; protein; 308 AA.
DE Clone Inestimalis nervous system associated protein SegID20.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 8.5%; Score 206.5; DB 8; Length 308;
Best Local Similarity 26.0%; Pred. No. 1.5e-10;
RESULT 1035
ID ADJ68929 standard; protein; 362 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID735.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.5%; Score 206.5; DB 7; Length 362;
Best Local Similarity 25.6%; Pred. No. 1.9e-10;
RESULT 1036
ID ADI82500 standard; protein; 362 AA.
DE Human modifier of p21 (MP21) protein sequence SegID66.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 8.5%; Score 206.5; DB 8; Length 362;
Best Local Similarity 25.6%; Pred. No. 1.9e-10;
RESULT 1037
ID ADP54036 standard; protein; 362 AA.
DE Human PRO protein sequence SEQ ID NO:12.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GERTH) GENENTECH INC.
Query Match 8.5%; Score 206.5; DB 8; Length 362;
Best Local Similarity 25.6%; Pred. No. 1.9e-10;

RESULT 1038
ID AAB60086 standard; protein; 274 AA.
DE Human transport protein TPPT-6.
PN WO200078953-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.5%; Score 206; DB 4; Length 274;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 1039
ID AAG64330 standard; protein; 274 AA.
DE Mitochondrial carrier 30.
PN WO200147982-A1.
PD 05-JUL-2001.
PA (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
Query Match 8.5%; Score 206; DB 4; Length 274;
Best Local Similarity 24.8%; Pred. No. 1.4e-10;
RESULT 1040
ID ADB64912 standard; protein; 274 AA.
DE Human protein encoded by clone PLACE60138840.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.5%; Score 206; DB 7; Length 274;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 1041
ID ADM05307 standard; protein; 274 AA.
DE Human protein of the invention SEQ ID NO:3992.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.5%; Score 206; DB 7; Length 274;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 1042
ID ADN24153 standard; protein; 290 AA.
DE Bacterial polypeptide #6806.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.5%; Score 206; DB 8; Length 290;
Best Local Similarity 23.5%; Pred. No. 1.6e-10;
RESULT 1043
ID ADN23884 standard; protein; 334 AA.
DE Bacterial polypeptide #6537.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.5%; Score 205.5; DB 8; Length 334;
Best Local Similarity 24.7%; Pred. No. 2.1e-10;
RESULT 1044
ID ADF55610 standard; protein; 286 AA.
DE Wheat uncoupling protein 1a (UCP1a).
PN JP2003245080-A.
PD 02-SEP-2003.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
Query Match 8.5%; Score 205; DB 7; Length 286;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 1045
ID AAM40265 standard; protein; 305 AA.
DE Human polypeptide SEQ ID NO 3410.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 205; DB 4; Length 305;
Best Local Similarity 23.8%; Pred. No. 2.1e-10;

RESULT 1046
ID ADM23204 standard; protein: 312 AA.
DE Bacterial polypeptide #5857.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
DE (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 8.5%; Score 205; DB 8; Length 312;
Best Local Similarity 25.2%; Pred. No. 2.2e-10;
RESULT 1047
ID ABG27643 standard; protein: 346 AA.
DE Novel human diagnostic protein #27634.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.5%; Score 205; DB 4; Length 346;
Best Local Similarity 22.4%; Pred. No. 2.5e-10;
RESULT 1048
ID AAB43682 standard; protein: 359 AA.
DE Human cancer associated protein sequence SEQ ID NO:1127.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.5%; Score 205; DB 3; Length 359;
Best Local Similarity 25.8%; Pred. No. 2.7e-10;
RESULT 1049
ID ADI16012 standard; protein: 361 AA.
DE Human PP 361.
PN WO2003008450-A1.
PD 30-JAN-2003.
PA (ITOH/) ITOH K.
Query Match
Best Local Similarity 8.5%; Score 205; DB 7; Length 361;
Best Local Similarity 25.8%; Pred. No. 2.7e-10;
RESULT 1050
ID ADJ68669 standard; protein: 361 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqId475.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
DE (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 8.5%; Score 205; DB 7; Length 361;
Best Local Similarity 25.8%; Pred. No. 2.7e-10;
RESULT 1051
ID ADJ68668 standard; protein: 361 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqId474.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
DE (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 8.5%; Score 205; DB 7; Length 361;
Best Local Similarity 25.8%; Pred. No. 2.7e-10;
RESULT 1052
ID ABP41590 standard; protein: 394 AA.
DE Human ovarian antigen HAZAR95, SEQ ID NO:2722.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 8.5%; Score 205; DB 5; Length 394;
Best Local Similarity 25.8%; Pred. No. 3.1e-10;
RESULT 1053
ID ADE09311 standard; protein: 472 AA.
DE Novel protein-related contig polypeptide sequence #377.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.5%; Score 205; DB 7; Length 472;
Best Local Similarity 25.8%; Pred. No. 4e-10;
RESULT 1054
ID AAG23667 standard; protein: 229 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27059.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 8.4%; Score 204.5; DB 3; Length 229;
Best Local Similarity 28.1%; Pred. No. 1.5e-10;
RESULT 1055
ID ABB42901 standard; peptide: 53 AA.
DE Peptide #10407 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 8.4%; Score 204; DB 4; Length 53;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
RESULT 1056
ID AAM36719 standard; protein: 53 AA.
DE Peptide #10756 encoded by probe for measuring placental gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 8.4%; Score 204; DB 4; Length 53;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
RESULT 1057
ID ABB26160 standard; protein: 53 AA.
DE Protein #8159 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 8.4%; Score 204; DB 4; Length 53;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
RESULT 1058
ID AAM76612 standard; protein: 53 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36918.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 8.4%; Score 204; DB 4; Length 53;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
RESULT 1059
ID AAM63799 standard; protein: 53 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35904.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 8.4%; Score 204; DB 4; Length 53;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
RESULT 1060
ID ABG58310 standard; peptide: 53 AA.
DE Human liver peptide, SEQ ID No 36958.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 8.4%; Score 204; DB 4; Length 53;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
RESULT 1061
ID ABG45847 standard; peptide: 53 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35512.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 8.4%; Score 204; DB 5; Length 53;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
RESULT 1062
ID ABO59738 standard; protein: 249 AA.
DE Human genome derived single exon protein #5972.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 8.4%; Score 204; DB 8; Length 249;
Best Local Similarity 28.6%; Pred. No. 1.9e-10;
RESULT 1063
ID ADD48795 standard; protein: 307 AA.
DE Rat Protein CAA06984, SEQ ID NO 14505.

PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.4%; Score 204; DB 7; Length 307;
Best Local Similarity 23.9%; Pred. No. 2.6e-10;
RESULT 1064
ID ADR89486 standard; protein; 307 AA.
DE Apoptosis-inducing protein, SEQ ID NO. 10.
PN W02004078112-A2.
PD 16-SEP-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 8.4%; Score 204; DB 8; Length 307;
Best Local Similarity 23.9%; Pred. No. 2.6e-10;
RESULT 1065
ID ABB5808 standard; protein; 317 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 816.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.4%; Score 204; DB 4; Length 317;
Best Local Similarity 22.8%; Pred. No. 2.7e-10;
RESULT 1066
ID AAE17974 standard; protein; 274 AA.
DE Human TZN07 full-length protein.
PN W0200202619-A1.
PD 10-JAN-2002.
PA (UTKU/) UTKU N.
Query Match 8.4%; Score 203; DB 5; Length 274;
Best Local Similarity 25.2%; Pred. No. 2.7e-10;
RESULT 1067
ID ADH7300 standard; protein; 274 AA.
DE Human novel T-cell protein TZN07 protein.
PN US2003219424-A1.
PD 27-NOV-2003.
PA (NALM/) NALM U.
Query Match 8.4%; Score 203; DB 8; Length 274;
Best Local Similarity 25.2%; Pred. No. 2.7e-10;
RESULT 1068
ID ADF55612 standard; protein; 286 AA.
DE Wheat uncoupling protein 1b (UCP1b).
PN JP2003245080-A.
PD 02-SEP-2003.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIRYUTSU SH.
Query Match 8.4%; Score 203; DB 7; Length 286;
Best Local Similarity 24.4%; Pred. No. 2.9e-10;
RESULT 1069
ID AAM93317 standard; protein; 361 AA.
DE Human polypeptide, SEQ ID NO: 2833.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.4%; Score 203; DB 4; Length 361;
Best Local Similarity 25.8%; Pred. No. 4.1e-10;
RESULT 1070
ID ADL30800 standard; protein; 361 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2833.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.4%; Score 203; DB 8; Length 361;
Best Local Similarity 25.8%; Pred. No. 4.1e-10;
RESULT 1071
ID AAB50419 standard; protein; 323 AA.
DE Human uncoupling protein peptide motif #24.
PN W0200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 202; DB 3; Length 323;
Best Local Similarity 27.5%; Pred. No. 4.4e-10;
RESULT 1072
ID AAG27858 standard; protein; 243 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32858.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.3%; Score 201.5; DB 3; Length 243;
Best Local Similarity 29.3%; Pred. No. 3.2e-10;
RESULT 1073
ID AAM93644 standard; protein; 287 AA.
DE Human polypeptide, SEQ ID NO: 3501.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.3%; Score 201.5; DB 4; Length 287;
Best Local Similarity 23.4%; Pred. No. 4.1e-10;
RESULT 1074
ID AAM39826 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 2971.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 201.5; DB 4; Length 287;
Best Local Similarity 23.4%; Pred. No. 4.1e-10;
RESULT 1075
ID AAB60116 standard; protein; 287 AA.
DE Human transport protein TPPT-36.
PN W0200078953-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.3%; Score 201.5; DB 4; Length 287;
Best Local Similarity 23.4%; Pred. No. 4.1e-10;
RESULT 1076
ID ADE55684 standard; protein; 287 AA.
DE Human Protein Q9UBX3, SEQ ID NO 1503.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.3%; Score 201.5; DB 7; Length 287;
Best Local Similarity 23.4%; Pred. No. 4.1e-10;
RESULT 1077
ID ADE55688 standard; protein; 287 AA.
DE Human Protein Q9UBX3, SEQ ID NO 1507.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.3%; Score 201.5; DB 7; Length 287;
Best Local Similarity 23.4%; Pred. No. 4.1e-10;
RESULT 1078
ID ADD45220 standard; protein; 287 AA.
DE Human Protein Q9UBX3, SEQ ID NO 10653.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.3%; Score 201.5; DB 8; Length 287;
Best Local Similarity 23.4%; Pred. No. 4.1e-10;
RESULT 1079
ID ADL31468 standard; protein; 287 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3501.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.3%; Score 201.5; DB 8; Length 287;
Best Local Similarity 23.4%; Pred. No. 4.1e-10;
RESULT 1080
ID AAM41612 standard; protein; 302 AA.
DE Human polypeptide SEQ ID NO 6543.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 201.5; DB 4; Length 302;
Best Local Similarity 23.4%; Pred. No. 4.4e-10;
RESULT 1081
ID AAB27019 standard; protein; 307 AA.

DE Protein associated with body weight disorders, SEQ ID NO: 56.
PN US6121017-A.
PD 19-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 201.5; DB 3; Length 307;
Best Local Similarity 22.9%; Pred. No. 4.5e-10;
RESULT 1082
ID ABO14803 standard; protein: 307 AA.
DE Mouse brown fat uncoupling protein (MUCP).
PN US6518402-B1.
PD 11-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 201.5; DB 7; Length 307;
Best Local Similarity 22.9%; Pred. No. 4.5e-10;
RESULT 1083
ID ADP18737 standard; protein: 307 AA.
DE Mouse lipid-storage promoter related protein, SEQ ID NO 31.
PN JP2004154135-A.
PD 03-JUN-2004.
PA (SUMO) SUMITOMO CHEM CO LTD.
PA (YAMA/) YAMANAKA S.
Query Match 8.3%; Score 201.5; DB 8; Length 307;
Best Local Similarity 22.9%; Pred. No. 4.5e-10;
RESULT 1084
ID AAB60658 standard; protein: 331 AA.
DE Human mitochondrial solute carrier protein hMSC-o.
PN CN1269409-A.
PD 11-OCT-2000.
PA (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
Query Match 8.3%; Score 201.5; DB 4; Length 331;
Best Local Similarity 24.2%; Pred. No. 5e-10;
RESULT 1085
ID ABR82448 standard; protein: 347 AA.
DE Human ARP28 polypeptide.
PN WO2003060148-A2.
PD 24-JUL-2003.
PA (SYST-) INST SYSTEMS BIOLOGY.
Query Match 8.3%; Score 201.5; DB 6; Length 347;
Best Local Similarity 24.2%; Pred. No. 5.4e-10;
RESULT 1086
ID ADQ74867 standard; protein: 347 AA.
DE Human androgen responsive prostate specific (ARP) polypeptide #10.
PN US2004137440-A1.
PD 15-JUN-2004.
PA (LINB/) LIN B.
Query Match 8.3%; Score 201.5; DB 8; Length 347;
Best Local Similarity 24.2%; Pred. No. 5.4e-10;
RESULT 1087
ID ADP25304 standard; protein: 347 AA.
DE PRO polypeptide SEQ ID NO:2482.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 8.3%; Score 201.5; DB 8; Length 347;
Best Local Similarity 24.2%; Pred. No. 5.4e-10;
RESULT 1088
ID ABG22635 standard; protein: 88 AA.
DE Novel human diagnostic protein #22626.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 201; DB 4; Length 88;
Best Local Similarity 68.5%; Pred. No. 7.7e-11;
RESULT 1089
ID AAM81591 standard; protein: 275 AA.
DE Human uncoupling protein 3 short form (UCP3sh).
PN WO9845438-A1.
PD 15-OCT-1998.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Query Match 8.3%; Score 201; DB 2; Length 275;
Best Local Similarity 25.7%; Pred. No. 4.3e-10;
RESULT 1090
ID ADS43946 standard; protein: 292 AA.

DE Bacterial polypeptide #22376.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.3%; Score 201; DB 8; Length 292;
Best Local Similarity 22.5%; Pred. No. 4.7e-10;
RESULT 1091
ID ABB66833 standard; protein: 360 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27291.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.3%; Score 201; DB 4; Length 360;
Best Local Similarity 28.1%; Pred. No. 6.4e-10;
RESULT 1092
ID ABB61169 standard; protein: 399 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10299.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.3%; Score 201; DB 4; Length 399;
Best Local Similarity 28.1%; Pred. No. 7.4e-10;
RESULT 1093
ID AAG41404 standard; protein: 212 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51510.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.3%; Score 200.5; DB 3; Length 212;
Best Local Similarity 28.4%; Pred. No. 3.2e-10;
RESULT 1094
ID AAM79274 standard; protein: 329 AA.
DE Human protein SEQ ID NO 1936.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 200.5; DB 4; Length 329;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1095
ID ABM83875 standard; protein: 336 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4124.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.3%; Score 200.5; DB 8; Length 336;
Best Local Similarity 24.2%; Pred. No. 6.4e-10;
RESULT 1096
ID ADS24273 standard; protein: 198 AA.
DE Bacterial polypeptide #13306.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.2%; Score 199.5; DB 8; Length 198;
Best Local Similarity 28.9%; Pred. No. 3.6e-10;
RESULT 1097
ID ADI62975 standard; protein: 311 AA.
DE Human apoptosis-associated protein SEQ ID 418.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 8.2%; Score 199.5; DB 7; Length 311;
Best Local Similarity 25.8%; Pred. No. 7.1e-10;
RESULT 1098
ID ADJ70417 standard; protein: 311 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2223.
PN WO2003087768-A2.

PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 8.2%; Score 199.5; DB 7; Length 311;
 Best Local Similarity 25.8%; Pred. No. 7.1e-10;
 RESULT 1099
 ID ADJ6525 standard; protein; 311 AA.
 DE Tricarboxylate transport protein for anti-cancer complex.
 PN W02004009622-A2.
 PD 29-JAN-2004.
 PA (CELL-) CELLZOME AG.
 Query Match 8.2%; Score 199.5; DB 8; Length 311;
 Best Local Similarity 25.8%; Pred. No. 7.1e-10;
 RESULT 1100
 ID ADS88198 standard; protein; 311 AA.
 DE Human protein of a TNF-alpha signalling pathway protein complex Seqid 53.
 PN W02004035783-A2.
 PD 29-APR-2004.
 PA (CELL-) CELLZOME AG.
 Query Match 8.2%; Score 199.5; DB 8; Length 311;
 Best Local Similarity 25.8%; Pred. No. 7.1e-10;
 RESULT 1101
 ID ADN21304 standard; protein; 319 AA.
 DE Bacterial polypeptide #3957.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 8.2%; Score 199.5; DB 8; Length 319;
 Best Local Similarity 24.7%; Pred. No. 7.4e-10;
 RESULT 1102
 ID ADN21303 standard; protein; 319 AA.
 DE Bacterial polypeptide #3956.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 8.2%; Score 199.5; DB 8; Length 319;
 Best Local Similarity 24.7%; Pred. No. 7.4e-10;
 RESULT 1103
 ID AAM83380 standard; protein; 275 AA.
 DE Human uncoupling protein UCP3S.
 PN W09850542-A1.
 PD 12-NOV-1998.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GRS MBH.
 Query Match 8.2%; Score 199; DB 2; Length 275;
 Best Local Similarity 25.7%; Pred. No. 6.6e-10;
 RESULT 1104
 ID AAY44293 standard; protein; 275 AA.
 DE Human uncoupling protein-3S.
 PN W09953953-A2.
 PD 28-OCT-1999.
 PA (UYVE-) UNIV VERMONT.
 Query Match 8.2%; Score 199; DB 3; Length 275;
 Best Local Similarity 25.7%; Pred. No. 6.6e-10;
 RESULT 1105
 ID AAY72343 standard; protein; 275 AA.
 DE Human uncoupling protein, UCP-3S.
 PN W0200078941-A2.
 PD 28-DEC-2000.
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 Query Match 8.2%; Score 199; DB 4; Length 275;
 Best Local Similarity 25.7%; Pred. No. 6.6e-10;
 RESULT 1106
 ID ABB81611 standard; protein; 275 AA.
 DE UCP3S protein sequence.

PN US2002065239-A1.
 PD 30-MAY-2002.
 PA (CAPL/) CAPLAN S L.
 PA (BOET/) BOETTCHER B R.
 PA (SLOS/) SLOSBERG E D.
 PA (CONN/) CONNELLY S.
 PA (KALE/) KALEKO M.
 PA (DESA/) DESAI V J.
 Query Match 8.2%; Score 199; DB 5; Length 275;
 Best Local Similarity 25.7%; Pred. No. 6.6e-10;
 RESULT 1107
 ID AAU09078 standard; protein; 284 AA.
 DE Human uncoupling protein, UCP-3S.
 PN W0200175131-A2.
 PD 11-OCT-2001.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 Query Match 8.2%; Score 199; DB 4; Length 284;
 Best Local Similarity 25.7%; Pred. No. 6.9e-10;
 RESULT 1108
 ID ADN19341 standard; protein; 284 AA.
 DE Bacterial polypeptide #1994.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 8.2%; Score 199; DB 8; Length 284;
 Best Local Similarity 23.5%; Pred. No. 6.9e-10;
 RESULT 1109
 ID ABB69107 standard; protein; 443 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 34113.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 8.2%; Score 199; DB 4; Length 443;
 Best Local Similarity 19.3%; Pred. No. 1.3e-09;
 RESULT 1110
 ID AAG28190 standard; protein; 200 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 33316.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 8.2%; Score 198.5; DB 3; Length 200;
 Best Local Similarity 29.7%; Pred. No. 4.6e-10;
 RESULT 1111
 ID ABB09514 standard; protein; 271 AA.
 DE Human uncoupling protein-1-like NOV6 protein, SEQ ID NO:26.
 PN W0200253742-A2.
 PD 11-JUL-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.2%; Score 198.5; DB 5; Length 271;
 Best Local Similarity 20.8%; Pred. No. 7.2e-10;
 RESULT 1112
 ID ADN21225 standard; protein; 272 AA.
 DE Bacterial polypeptide #3878.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 8.2%; Score 198.5; DB 8; Length 272;
 Best Local Similarity 24.4%; Pred. No. 7.2e-10;
 RESULT 1113
 ID AAE10330 standard; protein; 288 AA.
 DE Human transporter and ion channel-7 (TRICH-7) protein.
 PN W0200162923-A2.
 PD 30-AUG-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 8.2%; Score 198.5; DB 4; Length 288;
 Best Local Similarity 26.0%; Pred. No. 7.9e-10;

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RESULT 1114
ID ABB69700 standard; protein: 288 AA.
DE Human polypeptide SEQ ID NO 1747.
PN W0200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSECO INC.
Query Match
Best Local Similarity 8.2%; Score 198.5; DB 5; Length 288;
RESULT 1115
ID ADC39140 standard; protein: 288 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 82.
PN W02003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.2%; Score 198.5; DB 7; Length 288;
RESULT 1116
ID ADC39142 standard; protein: 288 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 84.
PN W02003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.2%; Score 198.5; DB 7; Length 288;
RESULT 1117
ID ABB78020 standard; protein: 246 AA.
DE Amino acid sequence of a human transporter.
PN W0200246212-A2.
PD 13-JUN-2002.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 8.2%; Score 198; DB 5; Length 246;
RESULT 1118
ID ADB64178 standard; protein: 246 AA.
DE Human protein encoded by clone CTONG20068360.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 8.2%; Score 198; DB 7; Length 246;
RESULT 1119
ID AAG07172 standard; protein: 241 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4223.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 8.2%; Score 197.5; DB 3; Length 241;
RESULT 1120
ID AAG76617 standard; protein: 335 AA.
DE Fruit fly uncoupling protein (UCP) protein sequence.
PN W0200242455-A2.
PD 30-MAY-2002.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match
Best Local Similarity 8.2%; Score 197.5; DB 5; Length 335;
RESULT 1121
ID ABR42158 standard; protein: 335 AA.
DE Drosophila uncoupling protein UCPY.
PN W02003037362-A2.
PD 08-MAY-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match
Best Local Similarity 8.2%; Score 197.5; DB 6; Length 335;
RESULT 1122
ID ABB56738 standard; protein: 335 AA.
DE Drosophila uncoupling protein UCPY SEQ ID NO:3.
PN W0200279478-A2.
PD 10-OCT-2002.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match
Best Local Similarity 8.2%; Score 197.5; DB 6; Length 335;
RESULT 1123
ID AAO23968 standard; protein: 335 AA.
DE Fruit fly uncoupling protein Y.
PN W02003061681-A2.
PD 31-JUL-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match
Best Local Similarity 8.2%; Score 197.5; DB 6; Length 335;
RESULT 1124
ID ADN21377 standard; protein: 374 AA.
DE Bacterial polypeptide #4030.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 8.1%; Score 197; DB 8; Length 374;
RESULT 1125
ID ADS24302 standard; protein: 197 AA.
DE Bacterial polypeptide #13335.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 8.1%; Score 196.5; DB 8; Length 197;
RESULT 1126
ID ADO10067 standard; protein: 271 AA.
DE Novel human protein NOV6.
PN US2004052806-A1.
PD 18-MAR-2004.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATY/) PATTERAJAN M.
PA (GROS/) GROSSE W M.
PA (LEPL/) LEPLLEY D M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILU/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S R.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ROTH/) ROTHENBERG M B.
PA (STON/) STONE D J.
PA (BOLD/) BOLDIG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (ANDE/) ANDERSON D W.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPFER R J.
PA (MILL/) MILLER C E.
PA (EISE/) EISEN A.
Query Match
Best Local Similarity 8.1%; Score 196.5; DB 8; Length 271;
RESULT 1127
ID ADS43938 standard; protein: 327 AA.
DE Bacterial polypeptide #22368.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
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PA (GOLD/) GOLDMAN B S.
Query Match 8.1%; Score 196.5; DB 8; Length 327;
Best Local Similarity 25.8%; Pred. No. 1.5e-09;
RESULT 1128
ID AAB64209 standard; protein: 335 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19419.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.1%; Score 196.5; DB 4; Length 335;
Best Local Similarity 23.4%; Pred. No. 1.5e-09;
RESULT 1129
ID AAM23997 standard; protein: 303 AA.
DE Mouse C5 gene product.
PN US5702902-A.
PD 30-DEC-1997.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.1%; Score 196; DB 2; Length 303;
Best Local Similarity 24.5%; Pred. No. 1.5e-09;
RESULT 1130
ID AAM89545 standard; protein: 303 AA.
DE Full length mouse C5 protein sequence.
PN US5853975-A.
PD 29-DEC-1998.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.1%; Score 196; DB 2; Length 303;
Best Local Similarity 24.5%; Pred. No. 1.5e-09;
RESULT 1131
ID AAY97997 standard; protein: 303 AA.
DE Mouse uncoupling protein C5, SEQ ID NO:37.
PN US6057109-A.
PD 02-MAY-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.1%; Score 196; DB 3; Length 303;
Best Local Similarity 24.5%; Pred. No. 1.5e-09;
RESULT 1132
ID AAB27017 standard; protein: 303 AA.
DE Protein associated with body weight disorders, SEQ ID NO: 37.
PN US6121017-A.
PD 19-SEP-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.1%; Score 196; DB 3; Length 303;
Best Local Similarity 24.5%; Pred. No. 1.5e-09;
RESULT 1133
ID AAB73297 standard; protein: 303 AA.
DE STCpa derived exothermicity relating gene protein #1.
PN JP2000354489-A.
PD 26-DEC-2000.
PA (KAGAKU GIUTTSU SHINKO JIGYODAN.
Query Match 8.1%; Score 196; DB 4; Length 303;
Best Local Similarity 22.2%; Pred. No. 1.5e-09;
RESULT 1134
ID ABO14801 standard; protein: 303 AA.
DE Mouse protein differentially expressed in obese/lean tissue C5.
PN US6518402-B1.
PD 11-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.1%; Score 196; DB 7; Length 303;
Best Local Similarity 24.5%; Pred. No. 1.5e-09;
RESULT 1135
ID AAB66875 standard; protein: 304 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27417.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.1%; Score 196; DB 4; Length 304;
Best Local Similarity 27.5%; Pred. No. 1.5e-09;
RESULT 1136
ID ADM19893 standard; protein: 305 AA.
DE Protein encoded by novel human channel/transporter gene #211.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 8.1%; Score 195.5; DB 4; Length 305;
Best Local Similarity 25.8%; Pred. No. 1.7e-09;
RESULT 1137
ID ADN22723 standard; protein: 392 AA.
DE Bacterial polypeptide #5376.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.1%; Score 195.5; DB 8; Length 392;
Best Local Similarity 22.2%; Pred. No. 2.4e-09;
RESULT 1138
ID AAB50394 standard; protein: 237 AA.
DE Human uncoupling protein #17.
PN W0200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.0%; Score 195; DB 3; Length 237;
Best Local Similarity 29.2%; Pred. No. 1.3e-09;
RESULT 1139
ID AAE04911 standard; protein: 237 AA.
DE Human transporter and ion channel-24 (TRICH-24) protein.
PN W0200146258-A2.
PD 28-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.0%; Score 195; DB 4; Length 237;
Best Local Similarity 29.2%; Pred. No. 1.3e-09;
RESULT 1140
ID ADM04515 standard; protein: 237 AA.
DE Human protein of the invention SEQ ID NO:3200.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.0%; Score 195; DB 7; Length 237;
Best Local Similarity 29.2%; Pred. No. 1.3e-09;
RESULT 1141
ID ADM04953 standard; protein: 237 AA.
DE Human protein of the invention SEQ ID NO:3638.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.0%; Score 195; DB 7; Length 237;
Best Local Similarity 29.2%; Pred. No. 1.3e-09;
RESULT 1142
ID ADC31772 standard; protein: 342 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1854.
PN W02003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.0%; Score 195; DB 7; Length 342;
Best Local Similarity 25.9%; Pred. No. 2.2e-09;
RESULT 1143
ID ADJ27213 standard; protein: 342 AA.
DE Human TRICH-45, SEQ ID 45.
PN W02004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.0%; Score 195; DB 8; Length 342;
Best Local Similarity 25.9%; Pred. No. 2.2e-09;
RESULT 1144
ID ADN24373 standard; protein: 374 AA.
DE Bacterial polypeptide #7026.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.0%; Score 195; DB 8; Length 374;

Best Local Similarity 27.7%; Pred. No. 2.5e-09;
RESULT 1145
ID AAG04867 standard; protein; 319 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1056.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 24.3%; Pred. No. 2.5e-09;
RESULT 1146
ID AAG04866 standard; protein; 336 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1055.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 24.3%; Pred. No. 2.6e-09;
RESULT 1147
ID AAG04865 standard; protein; 342 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1054.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 24.3%; Pred. No. 2.7e-09;
RESULT 1148
ID ABB64185 standard; protein; 374 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 19347.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 23.6%; Pred. No. 3.1e-09;
RESULT 1149
ID AAR91280 standard; protein; 303 AA.
DE Brown fat uncoupling protein C5 homologue.
PN W09605861-A1.
PD 29-FEB-1996.
PA (MILL-) MILLENIUM PHARM INC.
Query Match
Best Local Similarity 24.0%; Pred. No. 2.5e-09;
RESULT 1150
ID AAM85026 standard; protein; 317 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5275.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 21.0%; Pred. No. 3.4e-09;
RESULT 1151
ID AAM85024 standard; protein; 317 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5273.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 21.0%; Pred. No. 3.4e-09;
RESULT 1152
ID ADJ76309 standard; protein; 357 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1561.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 23.9%; Score 192.5; DB 8; Length 357;
RESULT 1153
ID ADP29877 standard; protein; 1148 AA.
DE Human secreted protein SEQ ID #644.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 20.6%; Pred. No. 2.3e-08;
RESULT 1154
ID AAY91479 standard; protein; 224 AA.
DE Human secreted protein sequence encoded by gene 29 SEQ ID NO:152.

PN W0200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 28.6%; Pred. No. 2.2e-09;
RESULT 1155
ID ADA56787 standard; protein; 224 AA.
DE Human secreted protein #69.
PN W02002102394-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 28.6%; Pred. No. 2.2e-09;
RESULT 1156
ID ADCT7406 standard; protein; 224 AA.
DE Human secreted protein - SEQ ID 679.
PN W02003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 28.6%; Pred. No. 2.2e-09;
RESULT 1157
ID ADD37843 standard; protein; 224 AA.
DE Human secreted protein #26.
PN W0200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 28.6%; Pred. No. 2.2e-09;
RESULT 1158
ID ADL71551 standard; protein; 225 AA.
DE Novel human secreted protein seqid 155.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSUTSUIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFLE/) LAFLEUR D W.
PA (WEIY/) WEI Y.
Query Match
Best Local Similarity 28.6%; Pred. No. 2.2e-09;
RESULT 1159
ID ADN23871 standard; protein; 337 AA.
DE Bacterial polypeptide #6524.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 24.6%; Pred. No. 4.1e-09;
RESULT 1160
ID ABO58867 standard; protein; 179 AA.
DE Human genome derived single exon protein #5101.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 30.6%; Pred. No. 1.8e-09;
RESULT 1161
ID ADN21404 standard; protein; 348 AA.
DE Bacterial polypeptide #4057.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
ID (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.9%; Score 191.5; DB 8; Length 348;
Best Local Similarity 25.1%; Pred. No. 4.8e-09;
RESULT 1162
ID ADI63105 standard; protein; 296 AA.
DE Human apoptosis-associated protein SEQ ID 548.
PN W02003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 7.9%; Score 191; DB 7; Length 296;
Best Local Similarity 23.4%; Pred. No. 4.2e-09;
RESULT 1163
ID AAY25740 standard; protein; 228 AA.
DE Human secreted protein encoded from gene 30.
PN W0938881-A1.
PD 05-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 190.5; DB 2; Length 228;
Best Local Similarity 29.0%; Pred. No. 3.2e-09;
RESULT 1164
ID ABB91885 standard; protein; 303 AA.
DE Herbicidially active polypeptide SEQ ID NO 1096.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (IPAR) BAYER AG.
Query Match 7.9%; Score 190.5; DB 5; Length 303;
Best Local Similarity 27.3%; Pred. No. 4.9e-09;
RESULT 1165
ID AAG17625 standard; protein; 331 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18719.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.9%; Score 190.5; DB 3; Length 331;
Best Local Similarity 18.5%; Pred. No. 5.6e-09;
RESULT 1166
ID AAG45478 standard; protein; 331 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57102.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.9%; Score 190.5; DB 3; Length 331;
Best Local Similarity 18.5%; Pred. No. 5.6e-09;
RESULT 1167
ID AAG53542 standard; protein; 725 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68177.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.9%; Score 190.5; DB 3; Length 725;
Best Local Similarity 29.4%; Pred. No. 1.8e-08;
RESULT 1168
ID AAG13164 standard; protein; 156 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12557.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.8%; Score 190; DB 3; Length 156;
Best Local Similarity 29.6%; Pred. No. 2e-09;
RESULT 1169
ID ADH22547 standard; protein; 235 AA.
DE Human transporter & ion channel (TRICH) protein SeqID45.
PN W02003093444-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 7.8%; Score 190; DB 8; Length 235;
Best Local Similarity 30.2%; Pred. No. 3.7e-09;
RESULT 1170
ID AAY29836 standard; protein; 256 AA.
DE Mouse uncoupling protein 3 polypeptide #3.
PN US952469-A.
PD 14-SEP-1999.
PA (TULA-) TULARIK INC.
Query Match 7.8%; Score 189.5; DB 2; Length 256;
Best Local Similarity 27.4%; Pred. No. 4.7e-09;

RESULT 1171
ID AAW85118 standard; protein; 256 AA.
DE A murine uncoupling protein designated mUCP3c.
PN US846779-A.
PD 08-DEC-1998.
PA (TULA-) TULARIK INC.
Query Match 7.8%; Score 189.5; DB 2; Length 256;
Best Local Similarity 27.4%; Pred. No. 4.7e-09;
RESULT 1172
ID AAY77454 standard; protein; 256 AA.
DE Murine mitochondrial uncoupling protein isoform mUCP3c.
PN US6025468-A.
PD 15-FEB-2000.
PA (TULA-) TULARIK INC.
Query Match 7.8%; Score 189.5; DB 3; Length 256;
Best Local Similarity 27.4%; Pred. No. 4.7e-09;
RESULT 1173
ID AAE04731 standard; protein; 256 AA.
DE Mouse uncoupling protein 3c (mUCP3c) protein.
PN US6248561-B1.
PD 19-JUN-2001.
PA (TULA-) TULARIK INC.
Query Match 7.8%; Score 189.5; DB 4; Length 256;
Best Local Similarity 27.4%; Pred. No. 4.7e-09;
RESULT 1174
ID AAW81592 standard; protein; 339 AA.
DE Protein encoded by human UCP3h gene reading frame 1.
PN W09845438-A1.
PD 15-OCT-1998.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Query Match 7.8%; Score 189.5; DB 2; Length 339;
Best Local Similarity 25.7%; Pred. No. 7.2e-09;
RESULT 1175
ID AAG11150 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9759.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.8%; Score 189; DB 3; Length 144;
Best Local Similarity 34.8%; Pred. No. 2.2e-09;
RESULT 1176
ID ABB65537 standard; protein; 287 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23403.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.8%; Score 188; DB 4; Length 287;
Best Local Similarity 25.0%; Pred. No. 7.7e-09;
RESULT 1177
ID AAG42777 standard; protein; 319 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53388.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.8%; Score 188; DB 3; Length 319;
Best Local Similarity 24.0%; Pred. No. 9.1e-09;
RESULT 1178
ID AAG42776 standard; protein; 336 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53387.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.8%; Score 188; DB 3; Length 336;
Best Local Similarity 24.0%; Pred. No. 9.8e-09;
RESULT 1179
ID AAG42775 standard; protein; 342 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53386.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.8%; Score 188; DB 3; Length 342;
Best Local Similarity 24.0%; Pred. No. 1e-08;
RESULT 1180
ID AAG41405 standard; protein; 177 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51511.
PN EP1033405-A2.
PD 06-SEP-2000.


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Query Match
Best Local Similarity 7.7%; Score 187.5; DB 3; Length 177;
RESULT 1181 31.3%; Pred. No. 4.2e-09;
ID ADN23392 standard; protein; 330 AA.
DE Bacterial polypeptide #6045.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 7.7%; Score 187.5; DB 8; Length 330;
RESULT 1182 28.1%; Pred. No. 1.1e-08;
ID ADO08614 standard; protein; 420 AA.
DE Ciona intestinalis nervous system associated protein SegID16.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match
Best Local Similarity 7.7%; Score 187; DB 8; Length 420;
RESULT 1183 23.2%; Pred. No. 1.7e-08;
ID ABB61816 standard; protein; 339 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12240.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 7.7%; Score 186.5; DB 4; Length 339;
RESULT 1184 21.3%; Pred. No. 1.4e-08;
ID ADR89484 standard; protein; 284 AA.
DE Apoptosis-inducing protein; SEQ ID 8.
PN WO2004078112-A2.
PD 16-SEP-2004.
PA (ASAH-) ASAH1 KASEI PHARMA CORP.
Query Match
Best Local Similarity 7.7%; Score 186; DB 8; Length 284;
RESULT 1185 23.5%; Pred. No. 1.2e-08;
ID ADS23492 standard; protein; 274 AA.
DE Bacterial polypeptide #12525.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 7.7%; Score 185.5; DB 8; Length 274;
RESULT 1186 25.5%; Pred. No. 1.2e-08;
ID ADD45218 standard; protein; 287 AA.
DE Rat Protein AJ223355, SEQ ID NO 10651.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (PARB ) BAYER AG.
Query Match
Best Local Similarity 7.7%; Score 185.5; DB 7; Length 287;
RESULT 1187 22.1%; Pred. No. 1.3e-08;
ID ADE55682 standard; protein; 287 AA.
DE Rat Protein AJ223355, SEQ ID NO 1501.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (PARB ) BAYER AG.
Query Match
Best Local Similarity 7.7%; Score 185.5; DB 7; Length 287;
RESULT 1188 22.1%; Pred. No. 1.3e-08;
ID ADE55686 standard; protein; 287 AA.
DE Rat Protein AJ223355, SEQ ID NO 1505.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (PARB ) BAYER AG.
Query Match
Best Local Similarity 7.7%; Score 185.5; DB 7; Length 287;
RESULT 1189 22.1%; Pred. No. 1.3e-08;
ID AAM79039 standard; protein; 299 AA.
DE Human protein SEQ ID NO 1701.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.7%; Score 185.5; DB 4; Length 299;
RESULT 1190 24.6%; Pred. No. 1.4e-08;
ID ABB61700 standard; protein; 303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11892.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 7.7%; Score 185.5; DB 4; Length 303;
RESULT 1191 23.9%; Pred. No. 1.4e-08;
ID AAG22959 standard; protein; 323 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26086.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 7.7%; Score 185.5; DB 3; Length 323;
RESULT 1192 22.3%; Pred. No. 1.6e-08;
ID ADS23455 standard; protein; 263 AA.
DE Bacterial polypeptide #12488.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 7.6%; Score 185; DB 8; Length 263;
RESULT 1193 23.1%; Pred. No. 1.3e-08;
ID ADN23063 standard; protein; 301 AA.
DE Bacterial polypeptide #5716.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 7.6%; Score 184.5; DB 8; Length 301;
RESULT 1194 22.9%; Pred. No. 1.8e-08;
ID AAB41707 standard; protein; 229 AA.
DE Human ORFX ORF1471 polypeptide sequence SEQ ID NO:2942.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.6%; Score 183.5; DB 3; Length 229;
RESULT 1195 34.6%; Pred. No. 1.5e-08;
ID AAG40152 standard; protein; 378 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49782.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 7.6%; Score 183.5; DB 3; Length 378;
RESULT 1196 21.1%; Pred. No. 3.1e-08;
ID AAG21416 standard; protein; 378 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23965.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 7.6%; Score 183.5; DB 3; Length 378;
RESULT 1197 21.1%; Pred. No. 3.1e-08;
```

RESULT 1197
PD AAG40151 standard; protein; 413 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49781.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.6%; Score 183.5; DB 3; Length 413;
Best Local Similarity 21.1%; Pred. No. 3.6e-08;
RESULT 1198
ID AAG21415 standard; protein; 413 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23964.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.6%; Score 183.5; DB 3; Length 413;
Best Local Similarity 21.1%; Pred. No. 3.6e-08;
RESULT 1199
ID ABB66885 standard; protein; 337 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 27447.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.6%; Score 183; DB 4; Length 337;
Best Local Similarity 25.6%; Pred. No. 2.9e-08;
RESULT 1200
ID AAE16774 standard; protein; 181 AA.
DE Human transporter and ion channel-11 (TRICH-11) protein.
PN WO200192304-A2.
PD 06-DEC-2001.
PA (INCYTE) INCYTE GENOMICS INC.
Query Match 7.5%; Score 182; DB 5; Length 181;
Best Local Similarity 28.8%; Pred. No. 1.4e-08;
RESULT 1201
ID AAG16698 standard; protein; 207 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17444.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.5%; Score 182; DB 3; Length 207;
Best Local Similarity 25.6%; Pred. No. 1.8e-08;
RESULT 1202
ID ADN18851 standard; protein; 299 AA.
DE Bacterial polypeptide #1504.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.5%; Score 182; DB 8; Length 299;
Best Local Similarity 25.3%; Pred. No. 3e-08;
RESULT 1203
ID ADN18921 standard; protein; 307 AA.
DE Bacterial polypeptide #1574.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.5%; Score 182; DB 8; Length 307;
Best Local Similarity 23.9%; Pred. No. 3.2e-08;
RESULT 1204
ID ABB64521 standard; protein; 300 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO: 20355.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.4%; Score 180.5; DB 4; Length 300;
Best Local Similarity 25.3%; Pred. No. 4.2e-08;
RESULT 1205
ID AAB3112 standard; protein; 188 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 170.
PN WO200058350-A1.

PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.4%; Score 180; DB 3; Length 188;
Best Local Similarity 25.7%; Pred. No. 2.4e-08;
RESULT 1206
ID AAM80023 standard; protein; 199 AA.
DE Human protein SEQ ID NO: 3669.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 180; DB 4; Length 199;
Best Local Similarity 25.7%; Pred. No. 2.6e-08;
RESULT 1207
ID AAE21226 standard; protein; 199 AA.
DE Human gene 13 encoded secreted protein HFVKC95, SEQ ID NO: 91.
PN WO200216390-A1.
PD 28-FEB-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.4%; Score 180; DB 5; Length 199;
Best Local Similarity 25.7%; Pred. No. 2.6e-08;
RESULT 1208
ID ABB64875 standard; protein; 199 AA.
DE Human albumin fusion protein #1550.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.4%; Score 180; DB 5; Length 199;
Best Local Similarity 25.7%; Pred. No. 2.6e-08;
RESULT 1209
ID ADU78142 standard; protein; 199 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO: 1624.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 7.4%; Score 180; DB 8; Length 199;
Best Local Similarity 25.7%; Pred. No. 2.6e-08;
RESULT 1210
ID ADS64665 standard; protein; 310 AA.
DE Saccharomyces cerevisiae transport protein Odc1p.
PN US2002155192-A1.
PD 24-OCT-2002.
PA (WALK/) WALKER J.
PA (RUNS/) RUNSWICK M.
PA (PALM/) PALMIERI F.
PA (PALM/) PALMIERI L.
PA (AGRI/) AGRIMI G.
Query Match 7.4%; Score 180; DB 5; Length 310;
Best Local Similarity 22.4%; Pred. No. 5e-08;
RESULT 1211
ID ADS44042 standard; protein; 310 AA.
DE Bacterial polypeptide #22472.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.4%; Score 180; DB 8; Length 310;
Best Local Similarity 22.4%; Pred. No. 5e-08;
RESULT 1212
ID AAG33253 standard; protein; 171 AA.
DE Zea mays protein fragment SEQ ID NO: 40262.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.4%; Score 179.5; DB 3; Length 171;
Best Local Similarity 29.1%; Pred. No. 2.3e-08;
RESULT 1213
ID AAB49666 standard; protein; 215 AA.
DE O. volvulus mitochondrial solute carrier (MSC) amino acid sequence.
PN CN1268568-A.
PD 04-OCT-2000.

PA (SCHR-) SOUTH CHINA RES CENT NAT HUMAN GENE GROU.
Query Match 7.4%; Score 179.5; DB 4; Length 215;
Best Local Similarity 25.1%; Pred. No. 3.2e-08;
RESULT 1214
ID ADN21399 standard; protein; 273 AA.
DE Bacterial polypeptide #4052.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.4%; Score 179; DB 8; Length 273;
Best Local Similarity 26.3%; Pred. No. 5.1e-08;
RESULT 1215
ID ABB60934 standard; protein; 297 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9594.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.4%; Score 178.5; DB 4; Length 297;
Best Local Similarity 25.7%; Pred. No. 6.5e-08;
RESULT 1216
ID ADN22545 standard; protein; 409 AA.
DE Bacterial polypeptide #5198.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.3%; Score 177.5; DB 8; Length 409;
Best Local Similarity 22.0%; Pred. No. 1.3e-07;
RESULT 1217
ID ABB59693 standard; protein; 240 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5871.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 176.5; DB 4; Length 240;
Best Local Similarity 28.8%; Pred. No. 7.3e-08;
RESULT 1218
ID AAB73298 standard; protein; 268 AA.
DE STUcPa derived exothermicity relating gene protein #2.
PN JP2000354489-A.
PD 26-DEC-2000.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 7.3%; Score 176.5; DB 4; Length 268;
Best Local Similarity 22.1%; Pred. No. 8.6e-08;
RESULT 1219
ID ABB63800 standard; protein; 303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18192.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 176.5; DB 4; Length 303;
Best Local Similarity 22.2%; Pred. No. 1e-07;
RESULT 1220
ID AAG06602 standard; protein; 223 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3433.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 176; DB 3; Length 223;
Best Local Similarity 27.8%; Pred. No. 7.3e-08;
RESULT 1221
ID AAB60101 standard; protein; 253 AA.
DE Human transport protein TPT-21.
PN WO200078953-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.3%; Score 176; DB 4; Length 253;

Best Local Similarity 23.0%; Pred. No. 8.8e-08;
RESULT 1222
ID ABB6398 standard; protein; 253 AA.
DE Human protein encoded by clone BRAMY20091230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 176; DB 7; Length 253;
Best Local Similarity 23.0%; Pred. No. 8.8e-08;
RESULT 1223
ID AAB32111 standard; protein; 194 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 169.
PN WO200058350-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.2%; Score 175.5; DB 3; Length 194;
Best Local Similarity 26.9%; Pred. No. 6.6e-08;
RESULT 1224
ID ABB6568 standard; protein; 280 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24396.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.2%; Score 175.5; DB 4; Length 280;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1225
ID ABB71693 standard; protein; 280 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41871.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.2%; Score 175.5; DB 4; Length 280;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1226
ID AAG40153 standard; protein; 318 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49783.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.2%; Score 175; DB 3; Length 318;
Best Local Similarity 23.5%; Pred. No. 1.5e-07;
RESULT 1227
ID AAG21417 standard; protein; 318 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23966.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.2%; Score 175; DB 3; Length 318;
Best Local Similarity 23.5%; Pred. No. 1.5e-07;
RESULT 1228
ID ADN20798 standard; protein; 272 AA.
DE Bacterial polypeptide #3451.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.2%; Score 174.5; DB 8; Length 272;
Best Local Similarity 25.3%; Pred. No. 1.4e-07;
RESULT 1229
ID ABB93491 standard; protein; 353 AA.
DE Herbicidally active polypeptide SEQ ID NO 2702.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 174.5; DB 5; Length 353;
Best Local Similarity 21.2%; Pred. No. 2e-07;
RESULT 1230
ID ADG87421 standard; protein; 243 AA.
DE Meloidogyne incognita dfti partial protein.
PN US2003150017-A1.
PD 07-AUG-2003.

PA (MESA/) MESA J R B.
PA (GRAH/) GRAHAM M W.
PA (FAIR/) FAIRBAIRN D J.
Query Match 7.1%; Score 173; DB 7; Length 243;
Best Local Similarity 27.0%; Pred. No. 1.6e-07;
RESULT 1231
ID ADN20907 standard; protein; 318 AA.
DE Bacterial polypeptide #3560.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 173; DB 8; Length 318;
Best Local Similarity 21.7%; Pred. No. 2.4e-07;
RESULT 1232
ID ADJ27204 standard; protein; 263 AA.
DE Human TRICH-36, SEQ ID 36.
PN WO2004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 172.5; DB 8; Length 263;
Best Local Similarity 27.2%; Pred. No. 2e-07;
RESULT 1233
ID AAM98199 standard; protein; 306 AA.
DE Potato malate oxoglutarate translocator.
PN WO906578-A2.
PD 11-FEB-1999.
PA (ZENE) ZENECA LTD.
Query Match 7.1%; Score 172.5; DB 2; Length 306;
Best Local Similarity 25.8%; Pred. No. 2.5e-07;
RESULT 1234
ID AAU01989 standard; protein; 174 AA.
DE Human secreted protein encoded by gene #25.
PN WO200123598-A1.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 171.5; DB 4; Length 174;
Best Local Similarity 26.7%; Pred. No. 1.3e-07;
RESULT 1235
ID ADN23953 standard; protein; 310 AA.
DE Bacterial polypeptide #6606.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 171; DB 8; Length 310;
Best Local Similarity 26.1%; Pred. No. 3.5e-07;
RESULT 1236
ID ADK62814 standard; protein; 324 AA.
DE Disease treating protein complex-derived protein #533.
PN BP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 7.1%; Score 171; DB 7; Length 324;
Best Local Similarity 22.8%; Pred. No. 3.8e-07;
RESULT 1237
ID ADS43810 standard; protein; 324 AA.
DE Bacterial polypeptide #22240.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 171; DB 8; Length 324;
Best Local Similarity 22.8%; Pred. No. 3.8e-07;

RESULT 1238
ID ADN19163 standard; protein; 298 AA.
DE Bacterial polypeptide #1816.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.0%; Score 170.5; DB 8; Length 298;
Best Local Similarity 23.1%; Pred. No. 3.7e-07;
RESULT 1239
ID ADS44092 standard; protein; 307 AA.
DE Bacterial polypeptide #22522.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.0%; Score 170.5; DB 8; Length 307;
Best Local Similarity 21.5%; Pred. No. 3.9e-07;
RESULT 1240
ID ADC39196 standard; protein; 323 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 138.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.0%; Score 170.5; DB 7; Length 323;
Best Local Similarity 24.6%; Pred. No. 4.2e-07;
RESULT 1241
ID ADE25081 standard; protein; 375 AA.
DE Plant growth associated protein seq id 56.
PN US2003188343-A1.
PD 02-OCT-2003.
PA (LYNX-) LYNX THERAPEUTICS INC.
Query Match 7.0%; Score 170.5; DB 7; Length 375;
Best Local Similarity 25.0%; Pred. No. 5.3e-07;
RESULT 1242
ID ADE08386 standard; protein; 218 AA.
DE Novel protein (useful for identifying genetic disorders) #541.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 168.5; DB 7; Length 218;
Best Local Similarity 25.1%; Pred. No. 3.6e-07;
RESULT 1243
ID AAM40817 standard; protein; 153 AA.
DE Human polypeptide SEQ ID NO 5748.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 168; DB 4; Length 153;
Best Local Similarity 27.1%; Pred. No. 2.4e-07;
RESULT 1244
ID ABG18922 standard; protein; 298 AA.
DE Novel human diagnostic protein #18913.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 168; DB 4; Length 298;
Best Local Similarity 24.1%; Pred. No. 6.4e-07;
RESULT 1245
ID AAM50925 standard; protein; 307 AA.
DE Yeast mitochondrial carrier protein YMC1.
PN WO200210342-A2.
PD 07-FEB-2002.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 6.9%; Score 167.5; DB 5; Length 307;
Best Local Similarity 21.2%; Pred. No. 7.5e-07;
RESULT 1246

ID ABG6657 standard; protein; 310 AA.
DE Rat mitochondrial energy transfer protein METP.
PN W0200240666-A2.
PD 23-MAY-2002.
PA (XENO-) XENON GENETICS INC.
Query Match 6.9%; Score 167.5; DB 5; Length 310;
Best Local Similarity 22.3%; Pred. No. 7.6e-07;
RESULT 1247

ID ADR86492 standard; protein; 329 AA.
DE Aspergillus fumigatus essential gene protein #542.
PN W02004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.9%; Score 167; DB 8; Length 329;
Best Local Similarity 26.1%; Pred. No. 9.3e-07;
RESULT 1248

ID ADM19896 standard; protein; 194 AA.
DE Protein encoded by novel human channel/transporter gene #214.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 166.5; DB 4; Length 194;
Best Local Similarity 26.7%; Pred. No. 4.7e-07;
RESULT 1249

ID ADA4816 standard; protein; 348 AA.
DE Rice protein conferring disease resistance in plants.
PN W02003000906-A2.
PD 03-JUN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match 6.9%; Score 166.5; DB 6; Length 348;
Best Local Similarity 24.2%; Pred. No. 1.1e-06;
RESULT 1250

ID AAM93934 standard; protein; 187 AA.
DE Human polypeptide, SEQ ID NO: 4110.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.9%; Score 166; DB 4; Length 187;
Best Local Similarity 24.6%; Pred. No. 4.9e-07;
RESULT 1251

ID ADL32077 standard; protein; 187 AA.
DE Human protein encoded by a full length cDNA clone SeqID 4110.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.9%; Score 166; DB 8; Length 187;
Best Local Similarity 24.6%; Pred. No. 4.9e-07;
RESULT 1252

ID AAM78413 standard; protein; 311 AA.
DE Human protein SEQ ID NO 1075.
PN W0200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 165.5; DB 4; Length 311;
Best Local Similarity 26.3%; Pred. No. 1.2e-06;
RESULT 1253

ID AAM39422 standard; protein; 311 AA.
DE Human polypeptide SEQ ID NO 2567.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 165.5; DB 4; Length 311;
Best Local Similarity 26.3%; Pred. No. 1.2e-06;
RESULT 1254

ID AAM79397 standard; protein; 326 AA.
DE Human protein SEQ ID NO 3043.
PN W0200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 165.5; DB 4; Length 326;
Best Local Similarity 26.3%; Pred. No. 1.3e-06;
RESULT 1255

ID AAG2960 standard; protein; 191 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26087.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 165; DB 3; Length 191;
Best Local Similarity 25.1%; Pred. No. 6.3e-07;
RESULT 1256

ID AAG08264 standard; protein; 216 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5730.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 165; DB 3; Length 216;
Best Local Similarity 24.9%; Pred. No. 7.6e-07;
RESULT 1257

ID AAG08263 standard; protein; 219 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5729.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 165; DB 3; Length 219;
Best Local Similarity 24.9%; Pred. No. 7.8e-07;
RESULT 1258

ID AAU31659 standard; protein; 229 AA.
DE Novel human secreted protein #2150.
PN W0200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 164.5; DB 4; Length 229;
Best Local Similarity 22.2%; Pred. No. 9.3e-07;
RESULT 1259

ID ADM20141 standard; protein; 162 AA.
DE Protein encoded by novel human channel/transporter gene #219 clone 2.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 164; DB 4; Length 162;
Best Local Similarity 32.3%; Pred. No. 6.2e-07;
RESULT 1260

ID ABB91992 standard; protein; 344 AA.
DE Herbicidally active polypeptide SEQ ID NO 1203.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.8%; Score 164; DB 5; Length 344;
Best Local Similarity 21.5%; Pred. No. 1.9e-06;
RESULT 1261

ID AAM41208 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 6139.
PN W0200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 163.5; DB 4; Length 360;
Best Local Similarity 21.4%; Pred. No. 2.3e-06;
RESULT 1262

ID AAB60106 standard; protein; 154 AA.
DE Human transport protein TPPT-26.
PN W0200078953-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 163; DB 4; Length 154;
Best Local Similarity 28.5%; Pred. No. 7.1e-07;
RESULT 1263

ID AAM93909 standard; protein; 187 AA.
DE Human polypeptide, SEQ ID NO: 4059.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.7%; Score 163; DB 4; Length 187;
Best Local Similarity 24.6%; Pred. No. 9.5e-07;
RESULT 1264

ID AAB49665 standard; protein; 187 AA.
DE Human mitochondrial solute carrier (MSC) amino acid sequence.
PN CN1268568-A.
PD 04-OCT-2000.

PA (SCHR-) SOUTH CHINA RES CENT NAT HUMAN GENE GROU.
Query Match 6.7%; Score 163; DB 4; Length 187;
Best Local Similarity 24.6%; Pred. No. 9.5e-07;
RESULT 1265
ID AAB98222 standard; protein; 187 AA.
DE Human mitochondrial solute carrier (hMSC) protein sequence.
PN CNI281895-A.
PD 31-JAN-2001.
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
Query Match 6.7%; Score 163; DB 4; Length 187;
Best Local Similarity 24.6%; Pred. No. 9.5e-07;
RESULT 1266
ID ADL32026 standard; protein; 187 AA.
DE Human protein encoded by a full length CDNA clone SeqID 4059.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 163; DB 8; Length 187;
Best Local Similarity 24.6%; Pred. No. 9.5e-07;
RESULT 1267
ID ADRI4667 standard; protein; 187 AA.
DE Human NF-kappaB pathway-associated protein SeqID668.
PN W0200406557-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 6.7%; Score 163; DB 8; Length 187;
Best Local Similarity 24.6%; Pred. No. 9.5e-07;
RESULT 1268
ID AAM82797 standard; protein; 193 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3046.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 163; DB 8; Length 193;
Best Local Similarity 24.6%; Pred. No. 1e-06;
RESULT 1269
ID AAM82798 standard; protein; 193 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3047.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 163; DB 8; Length 193;
Best Local Similarity 24.6%; Pred. No. 1e-06;
RESULT 1270
ID ADM1895 standard; protein; 227 AA.
DE Protein encoded by novel human channel/transporter gene #213.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 162.5; DB 4; Length 227;
Best Local Similarity 24.7%; Pred. No. 1.4e-06;
RESULT 1271
ID ADB65775 standard; protein; 225 AA.
DE Human protein encoded by clone UTERU20139760.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 162; DB 8; Length 225;
Best Local Similarity 26.1%; Pred. No. 1.6e-06;
RESULT 1272
ID ADS23506 standard; protein; 276 AA.
DE Bacterial polypeptide #12539.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 162; DB 8; Length 276;
Best Local Similarity 22.7%; Pred. No. 2.1e-06;
RESULT 1273

ID ABB60556 standard; protein; 296 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8460.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.7%; Score 162; DB 4; Length 296;
Best Local Similarity 27.6%; Pred. No. 2.4e-06;
RESULT 1274
ID ADN21548 standard; protein; 296 AA.
DE Bacterial polypeptide #4201.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 162; DB 8; Length 296;
Best Local Similarity 24.5%; Pred. No. 2.4e-06;
RESULT 1275
ID ADK64908 standard; protein; 300 AA.
DE Disease treating protein complex-derived protein #1562.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 6.7%; Score 162; DB 7; Length 300;
Best Local Similarity 23.3%; Pred. No. 2.4e-06;
RESULT 1276
ID ADN19089 standard; protein; 300 AA.
DE Bacterial polypeptide #1742.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 162; DB 8; Length 300;
Best Local Similarity 23.3%; Pred. No. 2.4e-06;
RESULT 1277
ID ADN20457 standard; protein; 313 AA.
DE Bacterial polypeptide #3110.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 162; DB 8; Length 313;
Best Local Similarity 20.5%; Pred. No. 2.6e-06;
RESULT 1278
ID ABB89456 standard; protein; 274 AA.
DE Human polypeptide SEQ ID NO 1832.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 161.5; DB 5; Length 274;
Best Local Similarity 19.0%; Pred. No. 2.3e-06;
RESULT 1279
ID AAG09948 standard; protein; 298 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8078.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 161.5; DB 3; Length 298;
Best Local Similarity 21.3%; Pred. No. 2.7e-06;
RESULT 1280
ID ADS23635 standard; protein; 402 AA.
DE Bacterial polypeptide #12668.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 21.6%; Score 160; DB 8; Length 402;
RESULT 1281
ID AAB40634 standard; protein; 176 AA.
DE Human OREF398 polypeptide sequence SEQ ID NO:796.
PN WO2005058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 26.7%; Score 159.5; DB 3; Length 176;
RESULT 1282
ID AAB98221 standard; protein; 176 AA.
DE Human mitochondrial solute carrier (IMSC-homologue) protein SEQ:7.
PN CN1281895-A.
PD 31-JAN-2001.
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
Query Match
Best Local Similarity 26.7%; Score 159.5; DB 4; Length 176;
RESULT 1283
ID AAO1988 standard; protein; 181 AA.
DE Gene #25 human secreted protein homologous amino acid sequence.
PN WO200123598-A1.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 28.5%; Score 159; DB 4; Length 181;
RESULT 1284
ID ADN21082 standard; protein; 274 AA.
DE Bacterial polypeptide #3735.
PN US200233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 21.5%; Score 159; DB 8; Length 274;
RESULT 1285
ID AAY96756 standard; protein; 301 AA.
DE A. terreus OREF14 Acetyl CoA transport protein.
PN WO20037629-A2.
PD 29-JUN-2000.
PA (WISC-) WISCONSIN ALUMNI RES FOUND.
Query Match
Best Local Similarity 23.8%; Score 159; DB 3; Length 301;
RESULT 1286
ID AAM50926 standard; protein; 329 AA.
DE Yeast mitochondrial carrier protein YMC2.
PN WO200210342-A2.
PD 07-FEB-2002.
PA (MED1-) MEDICAL RES COUNCIL.
Query Match
Best Local Similarity 20.1%; Score 159; DB 5; Length 329;
RESULT 1287
ID ADN18605 standard; protein; 329 AA.
DE Bacterial polypeptide #1458.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 20.1%; Score 159; DB 8; Length 329;
RESULT 1288
ID ADN21468 standard; protein; 336 AA.
DE Bacterial polypeptide #4121.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 19.6%; Score 157.5; DB 8; Length 336;
RESULT 1289
ID ABB78113 standard; peptide; 159 AA.
DE Amino acid sequence of tropoin C.
PN US2002072863-A1.
PD 13-JUN-2002.
PA (FUITSU) FUJITSU LTD.
Query Match
Best Local Similarity 28.9%; Score 157; DB 5; Length 159;
RESULT 1290
ID ABB83313 standard; protein; 159 AA.
DE Tropoin C.
PN US2002035434-A1.
PD 21-MAR-2002.
PA (FUITSU) FUJITSU LTD.
Query Match
Best Local Similarity 28.9%; Score 157; DB 5; Length 159;
RESULT 1291
ID ADS24131 standard; protein; 383 AA.
DE Bacterial polypeptide #13164.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 23.7%; Score 156.5; DB 8; Length 383;
RESULT 1292
ID ADN20775 standard; protein; 401 AA.
DE Bacterial polypeptide #3428.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 20.9%; Score 156.5; DB 8; Length 401;
RESULT 1293
ID AAG17626 standard; protein; 281 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18720.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 18.1%; Score 156; DB 3; Length 281;
RESULT 1294
ID AAG45479 standard; protein; 281 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57103.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 18.1%; Score 156; DB 3; Length 281;
RESULT 1295
ID ADS24342 standard; protein; 313 AA.
DE Bacterial polypeptide #13375.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 18.1%; Score 155.5; DB 8; Length 313;

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Best Local Similarity 21.4%; Pred. No. 1.1e-05;
RESULT 1296
ID AAG13165 standard; protein; 136 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12558.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 155; DB 3; Length 136;
Pred. No. 3.4e-06;
RESULT 1297
ID ABB64214 standard; protein; 155 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19434.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 6.4%; Score 155; DB 4; Length 155;
Pred. No. 4.1e-06;
RESULT 1298
ID AAG11152 standard; protein; 110 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9761.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 154; DB 3; Length 110;
Pred. No. 3.1e-06;
RESULT 1299
ID AAG18269 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19608.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 154; DB 3; Length 149;
Pred. No. 4.8e-06;
RESULT 1300
ID AAG07748 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5019.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 154; DB 3; Length 149;
Pred. No. 4.8e-06;
RESULT 1301
ID AAG52784 standard; protein; 163 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67136.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 154; DB 3; Length 163;
Pred. No. 5.5e-06;
RESULT 1302
ID AAG07747 standard; protein; 163 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5018.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 154; DB 3; Length 163;
Pred. No. 5.5e-06;
RESULT 1303
ID AAG18268 standard; protein; 163 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19607.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 154; DB 3; Length 163;
Pred. No. 5.5e-06;
RESULT 1304
ID ADS24327 standard; protein; 282 AA.
DE Bacterial polypeptide #13360.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.3%; Score 153.5; DB 8; Length 282;
Pred. No. 1.4e-05;
RESULT 1305
ID ABM73602 standard; protein; 306 AA.
DE DNA clone originating in barley containing SNP sequence #12.
PN W02003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match
Best Local Similarity 6.3%; Score 153.5; DB 7; Length 306;
Pred. No. 1.6e-05;
RESULT 1306
ID AAG22961 standard; protein; 170 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26088.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.3%; Score 153; DB 3; Length 170;
Pred. No. 7.3e-06;
RESULT 1307
ID AAE16768 standard; protein; 304 AA.
DE Human transporter and ion channel-5 (TRICH-5) protein.
PN W0200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.3%; Score 153; DB 5; Length 304;
Pred. No. 1.7e-05;
RESULT 1308
ID ADA55206 standard; protein; 176 AA.
DE Human protein, SEQ ID 2774.
PN EP1293568-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 6.3%; Score 152.5; DB 6; Length 176;
Pred. No. 8.6e-06;
RESULT 1309
ID AAM85048 standard; protein; 249 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:5297.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 6.3%; Score 152.5; DB 8; Length 249;
Pred. No. 1.4e-05;
RESULT 1310
ID ADS12980 standard; protein; 249 AA.
DE TRICH-3.
PN W02004083395-A2.
PD 30-SEP-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 6.3%; Score 152.5; DB 8; Length 249;
Pred. No. 1.4e-05;
RESULT 1311
ID ADN21547 standard; protein; 311 AA.
DE Bacterial polypeptide #4200.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.3%; Score 152; DB 8; Length 311;
Pred. No. 2.2e-05;
RESULT 1312
ID AAU29590 standard; protein; 299 AA.
DE Novel human secreted protein #81.
PN W0200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.2%; Score 151; DB 4; Length 299;
Pred. No. 2.6e-05;
RESULT 1313
ID AAG16699 standard; protein; 165 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17445.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.2%; Score 150.5; DB 3; Length 165;
Pred. No. 1.2e-05;
RESULT 1314
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ID AAB25780 standard; protein; 308 AA.
DE Human secreted protein SEQ ID #92.
PN WO200307491-A2.
PD 29-JUN-2000.
PA (GSEST) GENSET.
Query Match 6.2%; Score 150.5; DB 3; Length 308;
Best Local Similarity 22.8%; Pred. No. 3.1e-05;
RESULT 1315
ID AAB80951 standard; protein; 308 AA.
DE Human carnitine carrier related protein-1.
PN WO200100661-A2.
PD 04-JAN-2001.
PA (GSEST) GENSET.
Query Match 6.2%; Score 150.5; DB 4; Length 308;
Best Local Similarity 22.8%; Pred. No. 3.1e-05;
RESULT 1316
ID AAB38891 standard; protein; 308 AA.
DE Human polypeptide SEQ ID NO 2036.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 150.5; DB 4; Length 308;
Best Local Similarity 22.8%; Pred. No. 3.1e-05;
RESULT 1317
ID AAB75366 standard; protein; 308 AA.
DE Human secreted protein #25.
PN WO200100806-A2.
PD 04-JAN-2001.
PA (GSEST) GENSET.
Query Match 6.2%; Score 150.5; DB 4; Length 308;
Best Local Similarity 22.8%; Pred. No. 3.1e-05;
RESULT 1318
ID AAB66658 standard; protein; 308 AA.
DE Human mitochondrial energy transfer protein METP.
PN WO200240666-A2.
PD 23-MAY-2002.
PA (XENO-) XENON GENETICS INC.
Query Match 6.2%; Score 150.5; DB 5; Length 308;
Best Local Similarity 22.8%; Pred. No. 3.1e-05;
RESULT 1319
ID ADB64643 standard; protein; 308 AA.
DE Human protein encoded by clone LIVER20038000.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 6.2%; Score 150.5; DB 7; Length 308;
Best Local Similarity 22.8%; Pred. No. 3.1e-05;
RESULT 1320
ID ADP19167 standard; protein; 308 AA.
DE Human secreted polypeptide #18.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GSEST) GENSET SA.
Query Match 6.2%; Score 150.5; DB 8; Length 308;
Best Local Similarity 22.8%; Pred. No. 3.1e-05;
RESULT 1321
ID AAG38289 standard; protein; 178 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47215.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 150; DB 3; Length 178;
Best Local Similarity 26.4%; Pred. No. 1.5e-05;
RESULT 1322
ID AAG24015 standard; protein; 178 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27531.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 150; DB 3; Length 178;
Best Local Similarity 26.4%; Pred. No. 1.5e-05;
RESULT 1323
ID ADS24385 standard; protein; 228 AA.
DE Bacterial polypeptide #1318.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 150; DB 8; Length 228;
Best Local Similarity 26.1%; Pred. No. 2.2e-05;
RESULT 1324
ID ADL07541 standard; protein; 166 AA.
DE Human His-tagged Troponin C, Tnc.
PN CN1412312-A.
PD 23-APR-2003.
PA (CHON-) CHONGQING KANGERWEI PHARM IND CO LTD.
Query Match 6.2%; Score 149.5; DB 8; Length 166;
Best Local Similarity 27.3%; Pred. No. 1.5e-05;
RESULT 1325
ID ADA48002 standard; protein; 301 AA.
DE Rice protein conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.2%; Score 149.5; DB 6; Length 301;
Best Local Similarity 22.3%; Pred. No. 3.7e-05;
RESULT 1326
ID ABE23828 standard; protein; 349 AA.
DE Novel human diagnostic protein #23819.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 149.5; DB 4; Length 349;
Best Local Similarity 23.9%; Pred. No. 4.6e-05;
RESULT 1327
ID ABE21219 standard; protein; 356 AA.
DE Novel human diagnostic protein #21210.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 149.5; DB 4; Length 356;
Best Local Similarity 30.7%; Pred. No. 4.7e-05;
RESULT 1328
ID ADJ52168 standard; protein; 160 AA.
DE Human fast twitch skeletal muscle troponin C.
PN US2003119747-A1.
PD 26-JUN-2003.
PA (LANS/) LANSER M E.
Query Match 6.1%; Score 148.5; DB 7; Length 160;
Best Local Similarity 27.3%; Pred. No. 1.8e-05;
RESULT 1329
ID AAB44014 standard; protein; 132 AA.
DE Human cancer associated protein sequence SEQ ID NO:1459.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 148; DB 3; Length 132;
Best Local Similarity 36.7%; Pred. No. 1.5e-05;
RESULT 1330
ID AAB42653 standard; protein; 147 AA.
DE Human ORFX ORF2417 polypeptide sequence SEQ ID NO:4834.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 148; DB 3; Length 147;
Best Local Similarity 30.3%; Pred. No. 1.7e-05;
RESULT 1331
ID ADS44103 standard; protein; 328 AA.
DE Bacterial polypeptide #22533.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.1%; Score 148; DB 8; Length 328;
RESULT 1332
ID ABB65845 standard; protein; 426 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24327.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.1%; Score 148; DB 4; Length 426;
RESULT 1333
ID AAM22597 standard; protein; 160 AA.
DE Human fast twitch skeletal muscle troponin C.
PN W0200730085-A1.
PD 21-AUG-1997.
PA (CHIL-) CHILDRENS MEDICAL CENT.
Query Match
Best Local Similarity 6.1%; Score 147.5; DB 2; Length 160;
RESULT 1334
ID AAB00134 standard; protein; 160 AA.
DE Human fast twitch skeletal muscle Troponin subunit C.
PN W0200054770-A1.
PD 21-SEP-2000.
PA (BOST-) BOSTON LIFE SCI INC.
PA (CHIL-) CHILDRENS MEDICAL CENT.
Query Match
Best Local Similarity 6.1%; Score 147.5; DB 3; Length 160;
RESULT 1335
ID ABO63469 standard; protein; 160 AA.
DE Human Troponin C.
PN US2003083255-A1.
PD 01-MAY-2003.
PA (BOST-) BOSTON LIFE SCI INC.
Query Match
Best Local Similarity 6.1%; Score 147.5; DB 7; Length 160;
RESULT 1336
ID ABO01351 standard; protein; 160 AA.
DE Human fast-twitch skeletal muscle troponin subunit C protein.
PN US6589936-B1.
PD 08-JUL-2003.
PA (CHIL-) CHILDRENS MEDICAL CENT.
Query Match
Best Local Similarity 6.1%; Score 147.5; DB 7; Length 160;
RESULT 1337
ID ADD47323 standard; protein; 160 AA.
DE Human Protein NP_003270, SEQ ID NO 13017.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.1%; Score 147.5; DB 7; Length 160;
RESULT 1338
ID ADM19902 standard; protein; 175 AA.
DE Protein encoded by novel human channel/transporter gene #220.
PN W0200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.1%; Score 147.5; DB 4; Length 175;
RESULT 1339
ID ADN23491 standard; protein; 182 AA.
DE Bacterial polypeptide #6144.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 147.5; DB 8; Length 182;

Best Local Similarity 33.3%; Pred. No. 2.7e-05;
RESULT 1340
ID ADR46504 standard; protein; 172 AA.
DE Maize caltractin-like protein #1.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 6.1%; Score 147; DB 8; Length 172;
RESULT 1341
ID ADR46454 standard; protein; 172 AA.
DE Maize caltractin-like protein SEQ ID NO: 20.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 6.1%; Score 147; DB 8; Length 172;
RESULT 1342
ID AEM84204 standard; protein; 264 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:4453.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 6.1%; Score 147; DB 8; Length 264;
RESULT 1343
ID AAG51427 standard; protein; 340 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65269.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.1%; Score 147; DB 3; Length 340;
RESULT 1344
ID AAG04799 standard; protein; 350 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 964.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.1%; Score 147; DB 3; Length 350;
RESULT 1345
ID AAG13166 standard; protein; 105 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12559.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.0%; Score 146.5; DB 3; Length 105;
RESULT 1346
ID AAG45480 standard; protein; 221 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57104.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.0%; Score 146; DB 3; Length 221;
RESULT 1347
ID AAG17627 standard; protein; 221 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18721.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.0%; Score 146; DB 3; Length 221;
RESULT 1348
ID ABB06149 standard; protein; 245 AA.
DE Human NS protein sequence SEQ ID NO:241.
PN W0200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Query Match
Best Local Similarity 6.0%; Score 146; DB 5; Length 245;
RESULT 1349
ID AAG09949 standard; protein; 273 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8079.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 6.0%; Score 146; DB 3; Length 273;
Best Local Similarity 21.5%; Pred. No. 6.8e-05;
RESULT 1350
ID ADJ71109 standard; protein; 424 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2915.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.0%; Score 146; DB 7; Length 424;
Best Local Similarity 22.3%; Pred. No. 0.00013;
RESULT 1351
ID AAG21259 standard; protein; 166 AA.
DE Human gene 13 encoded secreted protein fragment, SEQ ID NO:125.
PN WO200216390-A1.
PD 28-FEB-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 145.5; DB 5; Length 166;
Best Local Similarity 24.8%; Pred. No. 3.6e-05;
RESULT 1352
ID ADM05740 standard; protein; 295 AA.
DE Human protein of the invention SEQ ID NO:4425.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.0%; Score 145.5; DB 7; Length 295;
Best Local Similarity 27.9%; Pred. No. 8.6e-05;
RESULT 1353
ID ADF70735 standard; protein; 300 AA.
DE Human uncoupling protein SEQ ID NO:2.
PN JP2003169683-A.
PD 17-JUN-2003.
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (RIKA) RIKAGAKU KENKYUSHO.
Query Match 6.0%; Score 145.5; DB 7; Length 300;
Best Local Similarity 27.9%; Pred. No. 8.8e-05;
RESULT 1354
ID ABM84205 standard; protein; 300 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4454.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.0%; Score 145.5; DB 8; Length 300;
Best Local Similarity 27.9%; Pred. No. 8.8e-05;
RESULT 1355
ID ADN18896 standard; protein; 300 AA.
DE Bacterial polypeptide #1549.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.0%; Score 145.5; DB 8; Length 300;
Best Local Similarity 26.4%; Pred. No. 8.8e-05;
RESULT 1356
ID AAG04800 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 965.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 145; DB 3; Length 322;
Best Local Similarity 21.7%; Pred. No. 0.00011;
RESULT 1357
ID AAU31108 standard; protein; 241 AA.
DE Novel human secreted protein #1599.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 144.5; DB 4; Length 241;
Best Local Similarity 21.2%; Pred. No. 7.9e-05;
RESULT 1358
ID ABP43648 standard; protein; 89 AA.

DE 19 cosmidg R30102:R29350:R27740.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 144; DB 5; Length 89;
Best Local Similarity 41.5%; Pred. No. 2e-05;
RESULT 1359
ID AAG24016 standard; protein; 164 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27532.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 143.5; DB 3; Length 164;
Best Local Similarity 26.3%; Pred. No. 5.5e-05;
RESULT 1360
ID AAG38290 standard; protein; 164 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47216.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 143.5; DB 3; Length 164;
Best Local Similarity 26.3%; Pred. No. 5.5e-05;
RESULT 1361
ID AAB60114 standard; protein; 300 AA.
DE Human transport protein TPPT-34.
PN WO200078953-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 143.5; DB 4; Length 300;
Best Local Similarity 27.9%; Pred. No. 0.00014;
RESULT 1362
ID ADC39144 standard; protein; 300 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 86.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 143.5; DB 7; Length 300;
Best Local Similarity 22.2%; Pred. No. 0.00014;
RESULT 1363
ID ADN33150 standard; protein; 282 AA.
DE Human transporter and ion channel (TRICH) protein SegID35.
PN WO2004035755-A2.
PD 29-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.9%; Score 143; DB 8; Length 282;
Best Local Similarity 24.8%; Pred. No. 0.00014;
RESULT 1364
ID AAG51428 standard; protein; 321 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65270.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 143; DB 3; Length 321;
Best Local Similarity 21.4%; Pred. No. 0.00017;
RESULT 1365
ID ADH32844 standard; protein; 279 AA.
DE Yeast smORF208-encoded polypeptide, SEQ ID NO:1302.
PN WO2002068693-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 142.5; DB 5; Length 279;
Best Local Similarity 22.9%; Pred. No. 0.00015;
RESULT 1366
ID ADN19612 standard; protein; 441 AA.
DE Bacterial polypeptide #2265.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 142.5; DB 8; Length 441;
Best Local Similarity 27.0%; Pred. No. 0.0003;
RESULT 1367
ID AAG30680 standard; protein; 151 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 36722.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 142; DB 3; Length 151;
Best Local Similarity 26.3%; Pred. No. 6.7e-05;
RESULT 1368
ID ABB63553 standard; protein; 155 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17451.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.9%; Score 142; DB 4; Length 155;
Best Local Similarity 25.0%; Pred. No. 7e-05;
RESULT 1369
ID ABB06148 standard; protein; 268 AA.
DE Human NS protein sequence SEQ ID NO:240.
PN W0200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Query Match 5.8%; Score 141.5; DB 5; Length 268;
Best Local Similarity 25.4%; Pred. No. 0.00018;
RESULT 1370
ID ADA46510 standard; protein; 299 AA.
DE Rice protein conferring disease resistance in plants.
PN W0200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.8%; Score 141.5; DB 6; Length 299;
Best Local Similarity 21.6%; Pred. No. 0.00021;
RESULT 1371
ID ADN19433 standard; protein; 318 AA.
DE Bacterial polypeptide #2086.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 5.8%; Score 141.5; DB 8; Length 318;
Best Local Similarity 20.1%; Pred. No. 0.00023;
RESULT 1372
ID ADN23484 standard; protein; 346 AA.
DE Bacterial polypeptide #6137.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 5.8%; Score 141.5; DB 8; Length 346;
Best Local Similarity 23.1%; Pred. No. 0.00026;
RESULT 1373
ID ADN23485 standard; protein; 346 AA.
DE Bacterial polypeptide #6138.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 5.8%; Score 141.5; DB 8; Length 346;
Best Local Similarity 23.1%; Pred. No. 0.00026;
RESULT 1374
ID AUS53097 standard; protein; 113 AA.
DE Human nucleic acid management-associated DKFZphes3_210m18 homologue #4.
PN W0200112659-A2.
PD 22-FEB-2001.
PA (GERH-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.8%; Score 141; DB 4; Length 113;
Best Local Similarity 33.7%; Pred. No. 5.4e-05;

RESULT 1375
ID ADR46446 standard; protein; 169 AA.
DE Rice caltractin-like protein SEQ ID NO: 12.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.8%; Score 141; DB 8; Length 169;
Best Local Similarity 28.0%; Pred. No. 9.9e-05;
RESULT 1376
ID ADR46500 standard; protein; 169 AA.
DE Rice caltractin-like protein #2.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.8%; Score 141; DB 8; Length 169;
Best Local Similarity 28.0%; Pred. No. 9.9e-05;
RESULT 1377
ID ADP99174 standard; protein; 208 AA.
DE Human transporter and ion channel (TRICH) protein - SEQ ID 39.
PN W02004048599-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 141; DB 8; Length 208;
Best Local Similarity 23.7%; Pred. No. 0.00014;
RESULT 1378
ID AAG08265 standard; protein; 153 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5721.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 140.5; DB 3; Length 153;
Best Local Similarity 25.7%; Pred. No. 9.5e-05;
RESULT 1379
ID AAP50078 standard; protein; 169 AA.
DE Sequence of the C-terminal of the mitochondrial uncoupling protein of rat
DE brown adipose tissue.
PN EP148686-A.
PD 17-JUL-1985.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (INSP) INST PASTEUR & GENETIC SYSTEMS.
Query Match 5.8%; Score 140.5; DB 1; Length 169;
Best Local Similarity 25.3%; Pred. No. 0.00011;
RESULT 1380
ID ABB08441 standard; protein; 223 AA.
DE Human OREX protein sequence SEQ ID NO:16864.
PN W0200192523-A2.
PD 06-DEC-2001.
PA (CTRA-) CTRAGEN CORP.
Query Match 5.8%; Score 140.5; DB 5; Length 223;
Best Local Similarity 23.1%; Pred. No. 0.00017;
RESULT 1381
ID AAG04801 standard; protein; 269 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 966.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 139.5; DB 3; Length 269;
Best Local Similarity 22.2%; Pred. No. 0.00028;
RESULT 1382
ID AAY95249 standard; protein; 150 AA.
DE Soybean calmodulin-4.
PN EP1018553-A1.
PD 12-JUL-2000.
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
Query Match 5.7%; Score 139; DB 3; Length 150;
Best Local Similarity 25.4%; Pred. No. 0.00013;
RESULT 1383
ID ADR46450 standard; protein; 158 AA.
DE Wheat caltractin-like protein SEQ ID NO: 16.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.7%; Score 139; DB 8; Length 158;
Best Local Similarity 28.0%; Pred. No. 0.00014;
RESULT 1384

ID ADR46503 standard; protein; 158 AA.
DE T aestivum caltracclin-like protein #2.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.7%; Score 139; DB 8; Length 158;
Best Local Similarity 28.0%; Pred. No. 0.00014;
RESULT 1385
ID ADR46502 standard; protein; 168 AA.
DE T aestivum caltracclin-like protein #1.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.7%; Score 139; DB 8; Length 168;
Best Local Similarity 28.0%; Pred. No. 0.00015;
RESULT 1386
ID ADR46448 standard; protein; 168 AA.
DE wheat caltracclin-like protein SEQ ID NO: 14.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.7%; Score 139; DB 8; Length 168;
Best Local Similarity 28.0%; Pred. No. 0.00015;
RESULT 1387
ID ADR46442 standard; protein; 170 AA.
DE Barley caltracclin-like protein SEQ ID NO: 8.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.7%; Score 139; DB 8; Length 170;
Best Local Similarity 28.0%; Pred. No. 0.00015;
RESULT 1388
ID ADR46494 standard; protein; 170 AA.
DE H vulgare caltracclin-like protein #1.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.7%; Score 139; DB 8; Length 170;
Best Local Similarity 28.0%; Pred. No. 0.00015;
RESULT 1389
ID AAM40677 standard; protein; 327 AA.
DE Human polypeptide SEQ ID NO 5608.
PN W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 139; DB 4; Length 327;
Best Local Similarity 23.9%; Pred. No. 0.00041;
RESULT 1390
ID AAM99655 standard; protein; 437 AA.
DE Human adenosine nucleotide translocator 4 protein derived from EST's.
PN W0907845-A1.
PD 18-FEB-1999.
PA (SMIK-) SMITHKLINE BEECHAM LAB PHARM.
Query Match 5.7%; Score 139; DB 2; Length 437;
Best Local Similarity 27.6%; Pred. No. 0.00064;
RESULT 1391
ID ADS24211 standard; protein; 231 AA.
DE Bacterial polypeptide #13244.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 5.7%; Score 138.5; DB 8; Length 231;
Best Local Similarity 25.9%; Pred. No. 0.00027;
RESULT 1392
ID ADQ18900 standard; protein; 161 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1719.
PN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 5.7%; Score 138; DB 8; Length 161;
Best Local Similarity 29.0%; Pred. No. 0.00018;
RESULT 1393
ID ADT02426 standard; protein; 247 AA.
DE Human tropoin I N-term-tropoin C.
PN US6475785-B1.
PD 05-NOV-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 5.7%; Score 138; DB 4; Length 247;
Best Local Similarity 29.0%; Pred. No. 0.00034;
RESULT 1394
ID ADT02428 standard; protein; 264 AA.
DE Human Tropoin I N-term-linker-tropoin C.
PN US6475785-B1.
PD 05-NOV-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 5.7%; Score 138; DB 4; Length 264;
Best Local Similarity 29.0%; Pred. No. 0.00037;
RESULT 1395
ID ADG14211 standard; protein; 371 AA.
DE Human tropoin I.
PN US2003176655-A1.
PD 18-SEP-2003.
PA (SHIQ-) SHI Q.
PA (SONG-) SONG Q.
Query Match 5.7%; Score 138; DB 7; Length 371;
Best Local Similarity 29.0%; Pred. No. 0.00062;
RESULT 1396
ID AAY25115 standard; protein; 390 AA.
DE Human cardiac tropoin I and tropoin C protein.
PN W09931235-A1.
PD 24-JUN-1999.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 5.7%; Score 138; DB 2; Length 390;
Best Local Similarity 29.0%; Pred. No. 0.00067;
RESULT 1397
ID ADG14206 standard; protein; 390 AA.
DE Human Tropoin I-tropoin C fusion protein.
PN US2003176655-A1.
PD 18-SEP-2003.
PA (SHIQ-) SHI Q.
PA (SONG-) SONG Q.
Query Match 5.7%; Score 138; DB 7; Length 390;
Best Local Similarity 29.0%; Pred. No. 0.00067;
RESULT 1398
ID AAR81571 standard; protein; 149 AA.
DE Porcine calmodulin.
PN US5498533-A.
PD 12-MAR-1996.
PA (UNIT-) UNIV WASHINGTON STATE RES FOUND.
Query Match 5.7%; Score 137.5; DB 2; Length 149;
Best Local Similarity 24.8%; Pred. No. 0.00018;
RESULT 1399
ID ADJ11392 standard; protein; 214 AA.
DE Rice protein modulated by post-transcriptional gene silencing Segid 28.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT-) ZHU T.
PA (WANG-) WANG X.
PA (CHANG-) CHANG H.
PA (BRIG-) BRIGGS S P.
PA (COOP-) COOPER B.
PA (GLAZ-) GLAZEBROOK J.
PA (GOLF-) GOLF S A.
PA (KATA-) KATAGIRI F.
PA (KREP-) KREPS J.
PA (MOUG-) MOUGHAMER T.
PA (PROV-) PROVART N.
PA (RICK-) RICE D.
Query Match 5.7%; Score 137.5; DB 7; Length 214;
Best Local Similarity 35.3%; Pred. No. 0.0003;
RESULT 1400
ID ADJ11738 standard; protein; 214 AA.

DE Rice protein modulated by post-transcriptional gene silencing SeqID 374.
PN US200313588-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBOOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKER D.
Query Match 5.7%; Score 137.5; DB 7; Length 214;
Best Local Similarity 35.3%; Pred. No. 0.0003;
RESULT 1401
ID ABM8079 standard; protein; 227 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81536, SEQ:2268.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.7%; Score 137.5; DB 8; Length 227;
Best Local Similarity 22.7%; Pred. No. 0.00033;
RESULT 1402
ID ADI21239 standard; protein; 233 AA.
DE Novel human protein #214.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 137.5; DB 7; Length 233;
Best Local Similarity 22.1%; Pred. No. 0.00034;
RESULT 1403
ID ABU11819 standard; protein; 128 AA.
DE Human MDDT polypeptide SEQ ID 766.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.7%; Score 137; DB 6; Length 128;
Best Local Similarity 31.4%; Pred. No. 0.00016;
RESULT 1404
ID ADL22715 standard; protein; 128 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 164.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.7%; Score 137; DB 7; Length 128;
Best Local Similarity 31.4%; Pred. No. 0.00016;
RESULT 1405
ID AAU30793 standard; protein; 425 AA.
DE Novel human secreted protein #1284.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 136.5; DB 4; Length 425;
Best Local Similarity 21.3%; Pred. No. 0.0011;
RESULT 1406
ID AAY95250 standard; protein; 150 AA.
DE Soybean calmodulin-5.
PN EPI018553-A1.
PD 12-JUL-2000.
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
Query Match 5.6%; Score 136; DB 3; Length 150;
Best Local Similarity 24.5%; Pred. No. 0.00025;
RESULT 1407
ID ABJ19405 standard; protein; 159 AA.
DE Human intracellular signalling protein - SEQ ID No 15.
PN WO2002101008-A2.
PD 19-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.6%; Score 136; DB 6; Length 159;
Best Local Similarity 27.1%; Pred. No. 0.00027;

RESULT 1408
ID AAG16479 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17141.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 135.5; DB 3; Length 215;
Best Local Similarity 25.6%; Pred. No. 0.00047;
RESULT 1409
ID AAG16478 standard; protein; 238 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17140.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 135.5; DB 3; Length 238;
Best Local Similarity 25.6%; Pred. No. 0.00055;
RESULT 1410
ID AAM80055 standard; protein; 126 AA.
DE Human protein SEQ ID NO 3701.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 135; DB 4; Length 126;
Best Local Similarity 34.5%; Pred. No. 0.00024;
RESULT 1411
ID ADA48048 standard; protein; 149 AA.
DE Rice protein conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.6%; Score 135; DB 6; Length 149;
Best Local Similarity 28.0%; Pred. No. 0.0003;
RESULT 1412
ID ABM74057 standard; protein; 192 AA.
DE DNA clone originating in barley containing SNP sequence #467.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNT-) UNIV JAPAN OKAYAMA.
Query Match 5.6%; Score 134.5; DB 7; Length 192;
Best Local Similarity 25.0%; Pred. No. 0.0005;
RESULT 1413
ID ABB92891 standard; protein; 550 AA.
DE Herbicidally active polypeptide SEQ ID NO 2102.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 134.5; DB 5; Length 550;
Best Local Similarity 27.8%; Pred. No. 0.0024;
RESULT 1414
ID AAG36518 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44764.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 134; DB 3; Length 113;
Best Local Similarity 28.0%; Pred. No. 0.00025;
RESULT 1415
ID AAG46104 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60713.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 134; DB 3; Length 113;
Best Local Similarity 28.0%; Pred. No. 0.00025;
RESULT 1416
ID AAG38371 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47329.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 134; DB 3; Length 113;
Best Local Similarity 28.0%; Pred. No. 0.00025;
RESULT 1417
ID AAG09211 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7054.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 134; DB 3; Length 113;

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Best Local Similarity 28.0%; Pred. No. 0.00025;
RESULT 1418
ID AAG19560 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21407.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 113;
Pred. No. 0.00025;
RESULT 1419
ID AAG36789 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45135.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 113;
Pred. No. 0.00025;
RESULT 1420
ID AAG48201 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60845.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 113;
Pred. No. 0.00025;
RESULT 1421
ID AAG38439 standard; protein; 123 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47423.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 123;
Pred. No. 0.00028;
RESULT 1422
ID AAY77954 standard; protein; 136 AA.
DE A. thaliana environmental stress tolerance related protein.
PN WQ200008187-A2.
PD 17-FEB-2000.
PA (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 136;
Pred. No. 0.00033;
RESULT 1423
ID AAG40533 standard; protein; 146 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50304.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 146;
Pred. No. 0.00037;
RESULT 1424
ID AAG19559 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21406.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 149;
Pred. No. 0.00038;
RESULT 1425
ID AAG36788 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45134.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 149;
Pred. No. 0.00038;
RESULT 1426
ID AAG48103 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60712.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 149;
Pred. No. 0.00038;
RESULT 1427
ID AAG09210 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7053.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 134; DB 3; Length 149;
Pred. No. 0.00038;
RESULT 1428
Best Local Similarity 28.0%; Pred. No. 0.00038;
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
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Query Match
Best Local Similarity 5.5%; Score 133.5; DB 8; Length 291;
RESULT 1438
ID ABB93127 standard; protein; 378 AA.
DE Herbicidally active polypeptide SEQ ID NO 2338.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 5.5%; Score 133.5; DB 5; Length 378;
RESULT 1439
ID ADN22744 standard; protein; 145 AA.
DE Bacterial polypeptide #5397.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 145;
RESULT 1440
ID ADR46488 standard; protein; 167 AA.
DE A thaliana caltracin-like protein #1.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 167;
RESULT 1441
ID ADR46436 standard; protein; 167 AA.
DE A thaliana caltracin-like protein SEQ ID NO: 2.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 167;
RESULT 1442
ID AAG41732 standard; protein; 169 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51959.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.5%; Score 133; DB 3; Length 169;
RESULT 1443
ID ADN73639 standard; protein; 169 AA.
DE Thale cress8 protein repressed in E2Fa/Dpa expressing plants SeqID 1534.
PN W02004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 169;
RESULT 1444
ID ADR46438 standard; protein; 169 AA.
DE A thaliana caltracin-like protein SEQ ID NO: 4.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 169;
RESULT 1445
ID ADR46489 standard; protein; 169 AA.
DE A thaliana caltracin-like protein #2.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 169;
RESULT 1446
ID ADS23497 standard; protein; 262 AA.
DE Bacterial polypeptide #12530.
PN US2003233675-A1.
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PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 262;
RESULT 1447
ID ADN19827 standard; protein; 297 AA.
DE Bacterial polypeptide #2480.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.5%; Score 133; DB 8; Length 297;
RESULT 1448
ID AAY31930 standard; protein; 112 AA.
DE Barley brittle-1 partial polypeptide.
PN W09949047-A2.
PD 30-SEP-1999.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 5.5%; Score 132.5; DB 2; Length 112;
RESULT 1449
ID AAB41602 standard; protein; 125 AA.
DE Human ORFX ORF1366 polypeptide sequence SEQ ID NO:2732.
PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.5%; Score 132.5; DB 3; Length 125;
RESULT 1450
ID AAB50387 standard; protein; 162 AA.
DE Human uncoupling protein #10.
PN W0200061614-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMANA GENOME SCI INC.
Query Match
Best Local Similarity 5.5%; Score 132.5; DB 3; Length 162;
RESULT 1451
ID AAY50797 standard; protein; 149 AA.
DE Human calmodulin/NEF protein binding inhibitor 2.
PN W09957136-A2.
PD 11-NOV-1999.
PA (SCHO/) SCHOTT M.
PA (SCHO/) SCHORR J.
PA (ANTZ/) ANTZ C.
Query Match
Best Local Similarity 5.4%; Score 132; DB 3; Length 149;
RESULT 1452
ID AAG24433 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 28103.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.4%; Score 132; DB 3; Length 181;
RESULT 1453
ID ABB41526 standard; protein; 176 AA.
DE Human ovarian antigen HAPOW35, SEQ ID NO:2658.
PN W0200200677-A1.
PD 03-JUN-2002.
PA (HUMA-) HUMANA GENOME SCI INC.
Query Match
Best Local Similarity 5.4%; Score 131.5; DB 5; Length 176;
RESULT 1454
ID AAG16480 standard; protein; 188 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17142.
PN EP1033405-A2.
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PD 06-SEP-2000.
Query Match 5.4%; Score 131.5; DB 3; Length 188;
Best Local Similarity 25.6%; Pred. No. 0.00092;
RESULT 1455
ID AAG2935 standard; protein; 113 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26052.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 131; DB 3; Length 113;
Best Local Similarity 26.9%; Pred. No. 0.00048;
RESULT 1456
ID ABM73621 standard; protein; 119 AA.
DE DNA clone originating in barley containing SNP sequence #31.
PN W0200305787-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 5.4%; Score 131; DB 7; Length 119;
Best Local Similarity 26.9%; Pred. No. 0.00052;
RESULT 1457
ID ADA48230 standard; protein; 130 AA.
DE Rice protein conferring disease resistance in plants.
PN W0200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.4%; Score 131; DB 6; Length 130;
Best Local Similarity 26.9%; Pred. No. 0.00059;
RESULT 1458
ID ADR46440 standard; protein; 142 AA.
DE B napus caltractin-like protein SEQ ID NO: 6.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.4%; Score 131; DB 8; Length 142;
Best Local Similarity 27.0%; Pred. No. 0.00068;
RESULT 1459
ID ADR46490 standard; protein; 142 AA.
DE B napus caltractin-like protein #1.
PN W02004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.4%; Score 131; DB 8; Length 142;
Best Local Similarity 27.0%; Pred. No. 0.00068;
RESULT 1460
ID AAG2934 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26051.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 131; DB 3; Length 149;
Best Local Similarity 26.9%; Pred. No. 0.00073;
RESULT 1461
ID ADA4604 standard; protein; 149 AA.
DE Rice protein conferring disease resistance in plants.
PN W02003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.4%; Score 131; DB 6; Length 149;
Best Local Similarity 26.9%; Pred. No. 0.00073;
RESULT 1462
ID AAG2933 standard; protein; 182 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26050.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 131; DB 3; Length 182;
Best Local Similarity 26.9%; Pred. No. 0.00098;
RESULT 1463
ID AAG0950 standard; protein; 262 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8080.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 131; DB 3; Length 262;
Best Local Similarity 21.3%; Pred. No. 0.0017;
RESULT 1464
ID AAM40554 standard; protein; 304 AA.

DE Human polypeptide SEQ ID NO 5485.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 131; DB 4; Length 304;
Best Local Similarity 21.9%; Pred. No. 0.0021;
RESULT 1465
ID AAG50078 standard; protein; 315 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63422.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 131; DB 3; Length 315;
Best Local Similarity 20.6%; Pred. No. 0.0022;
RESULT 1466
ID ADN3126 standard; protein; 186 AA.
DE Human transporter and ion channel (TRICH) protein SeqID1.
PN W02004035755-A2.
PD 29-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.4%; Score 130.5; DB 8; Length 186;
Best Local Similarity 23.7%; Pred. No. 0.0011;
RESULT 1467
ID ADN21509 standard; protein; 257 AA.
DE Bacterial polypeptide #4162.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.4%; Score 130.5; DB 8; Length 257;
Best Local Similarity 29.3%; Pred. No. 0.0018;
RESULT 1468
ID AAV30158 standard; protein; 298 AA.
DE Novel human secreted protein #649.
PN W0200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 130.5; DB 4; Length 298;
Best Local Similarity 25.3%; Pred. No. 0.0023;
RESULT 1469
ID ADP99127 standard; protein; 386 AA.
DE C. albicans specific gene, orf19.5052, protein sequence.
PN W02004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.4%; Score 130.5; DB 8; Length 386;
Best Local Similarity 18.4%; Pred. No. 0.0034;
RESULT 1470
ID AAG38372 standard; protein; 98 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47330.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 130; DB 3; Length 98;
Best Local Similarity 29.1%; Pred. No. 0.00048;
RESULT 1471
ID AAG19561 standard; protein; 98 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21408.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 130; DB 3; Length 98;
Best Local Similarity 29.1%; Pred. No. 0.00048;
RESULT 1472
ID AAG3619 standard; protein; 98 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44765.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 130; DB 3; Length 98;
Best Local Similarity 29.1%; Pred. No. 0.00048;
RESULT 1473
ID AAG09212 standard; protein; 98 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 7055.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 130; DB 3; Length 98;
Best Local Similarity 29.1%; Pred. No. 0.00046;
RESULT 1474
ID AAG38440 standard; protein; 108 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47424.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 130; DB 3; Length 108;
Best Local Similarity 29.1%; Pred. No. 0.00036;
RESULT 1475
ID AAG40534 standard; protein; 131 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50305.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 130; DB 3; Length 131;
Best Local Similarity 29.1%; Pred. No. 0.00075;
RESULT 1476
ID AAY50796 standard; protein; 146 AA.
DE Human calmodulin/NEF protein binding inhibitor 1.
PN MO9957136-A2.
PD 11-NOV-1999.
PA (SCHO/) SCHOOT M.
PA (SCHO/) SCHORR J.
PA (ANTZ/) ANTZ C.
Query Match 5.4%; Score 130; DB 3; Length 146;
Best Local Similarity 26.9%; Pred. No. 0.00086;
RESULT 1477
ID ADN19493 standard; protein; 149 AA.
DE Bacterial polypeptide #2146.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.4%; Score 130; DB 8; Length 149;
Best Local Similarity 28.0%; Pred. No. 0.0009;
RESULT 1478
ID AAP80162 standard; protein; 151 AA.
DE Biosynthetic multifunctional protein.
PN MO809344-A.
PD 01-DEC-1988.
PA (CREA-) CREATIVE BIOMOLECULES INC.
Query Match 5.4%; Score 130; DB 1; Length 151;
Best Local Similarity 25.8%; Pred. No. 0.00092;
RESULT 1479
ID AAY97294 standard; protein; 297 AA.
DE Lipid associated protein (LIPAP) 3735780CD1.
PN MO200049043-A2.
PD 24-AUG-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.4%; Score 130; DB 3; Length 297;
Best Local Similarity 21.6%; Pred. No. 0.0025;
RESULT 1480
ID AAM38768 standard; protein; 297 AA.
DE Human polypeptide SEQ ID NO 1913.
PN MO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSE INC.
Query Match 5.4%; Score 130; DB 4; Length 297;
Best Local Similarity 21.6%; Pred. No. 0.0025;
RESULT 1481
ID AAB60090 standard; protein; 297 AA.
DE Human transport protein TPT-10.
PN MO200078953-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.4%; Score 130; DB 4; Length 297;
Best Local Similarity 21.6%; Pred. No. 0.0025;
RESULT 1482
ID AAR78526 standard; protein; 375 AA.
DE GST-calmodulin fusion protein.
PN JP07126297-A.
PD 16-MAY-1995.
PA (SAGA) SAGAMI CHEM RES CENTRE.
Query Match 5.4%; Score 130; DB 2; Length 375;
Best Local Similarity 22.4%; Pred. No. 0.0036;
RESULT 1483
ID AAG43187 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53950.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 129.5; DB 3; Length 215;
Best Local Similarity 23.0%; Pred. No. 0.0017;
RESULT 1484
ID AAG07956 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5305.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 129.5; DB 3; Length 215;
Best Local Similarity 23.0%; Pred. No. 0.0017;
RESULT 1485
ID ADN73189 standard; protein; 215 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 1084.
PN MO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 5.3%; Score 129.5; DB 8; Length 215;
Best Local Similarity 23.0%; Pred. No. 0.0017;
RESULT 1486
ID AAM85049 standard; protein; 227 AA.
DE Human diagnostic and therapeutic pproetin SEQ ID NO:5298.
PN MO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.3%; Score 129.5; DB 8; Length 227;
Best Local Similarity 25.1%; Pred. No. 0.0019;
RESULT 1487
ID ADP99176 standard; protein; 259 AA.
DE Human transporter and ion channel (TRICH) protein - SEQ ID 41.
PN MO200404859-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.3%; Score 129.5; DB 8; Length 259;
Best Local Similarity 21.8%; Pred. No. 0.0023;
RESULT 1488
ID AAB61777 standard; protein; 450 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12123.
PN MO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 129.5; DB 4; Length 450;
Best Local Similarity 22.0%; Pred. No. 0.0053;
RESULT 1489
ID ADN04466 standard; protein; 97 AA.
DE Antisporiatric protein sequence #426.
PN MO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.3%; Score 129; DB 8; Length 97;
Best Local Similarity 26.7%; Pred. No. 0.00059;
RESULT 1490
ID ADP17767 standard; protein; 149 AA.
DE Differentially expressed protein lnt2, SEQ ID 2.
PN MO2004015390-A2.
PD 19-FEB-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.3%; Score 129; DB 8; Length 149;
Best Local Similarity 26.7%; Pred. No. 0.0011;
RESULT 1491
ID ADN19687 standard; protein; 271 AA.
DE Bacterial polypeptide #2340.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.3%; Score 129; DB 8; Length 271;
RESULT 1492
ID A0543461 standard; protein; 178 AA.
DE Bacterial polypeptide #21891.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 5.3%; Score 128.5; DB 8; Length 178;
RESULT 1493
ID A0K00685 standard; protein; 113 AA.
DE HOMO protein #31.
PN WO2004014946-A1.
PD 19-FEB-2004.
PA (MEMO-) MEMORGEN LTD.
Query Match
Best Local Similarity 5.3%; Score 128; DB 8; Length 113;
RESULT 1494
ID AAU31107 standard; protein; 125 AA.
DE Novel human secreted protein #1598.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.3%; Score 128; DB 4; Length 125;
RESULT 1495
ID ABB83067 standard; protein; 148 AA.
DE Rat calmodulin amino acid sequence.
PN EP1209167-A1.
PD 29-MAY-2002.
PA (OKAZ-) OKAZAKI NAT RES INST.
Query Match
Best Local Similarity 5.3%; Score 128; DB 5; Length 148;
RESULT 1496
ID ADE63418 standard; protein; 148 AA.
DE Rat protein P02593, SEQ ID NO 9357.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 5.3%; Score 128; DB 7; Length 148;
RESULT 1497
ID ADE57182 standard; protein; 148 AA.
DE Human Protein P02593, SEQ ID NO 3043.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 5.3%; Score 128; DB 7; Length 148;
RESULT 1498
ID AAR04583 standard; protein; 149 AA.
DE Recombinant calmodulin.
PN JP02092286-A.
PD 03-APR-1990.
PA (KIRI) KIRIN BREWERY KK.
Query Match
Best Local Similarity 5.3%; Score 128; DB 2; Length 149;
RESULT 1499
ID AAR78523 standard; protein; 149 AA.

DE Human calmodulin protein.
PN JP07126297-A.
PD 16-MAY-1995.
PA (SAGA) SAGAMI CHEM RES CENTRE.
Query Match
Best Local Similarity 5.3%; Score 128; DB 2; Length 149;
RESULT 1500
ID AAG03832 standard; protein; 149 AA.
DE Human secreted protein, SEQ ID NO: 7913.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSTRT.
Query Match
Best Local Similarity 5.3%; Score 128; DB 3; Length 149;
RESULT 1501
ID AAG03832 standard; protein; 149 AA.
DE Human secreted protein, SEQ ID NO: 7913.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSTRT.
Query Match
Best Local Similarity 5.3%; Score 128; DB 3; Length 149;

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OM protein - protein search, using sw model

Run on: August 5, 2005, 20:22:41 ; Search time 19 seconds

(without alignments)
2375.035 Million cell updates/sec

Title: US-10-063-565-58

Perfect score: 2423

Sequence: 1 MCLCLGVPIGAGTGFQY.....VSISYVYENLKITLGQSR 469

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79: *
1: Dirl: *
2: Dirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1494	61.7	475	2	T50686	peroxisomal Ca-dep
2	1177.5	48.6	588	2	T22688	hypothetical prote
3	1030.5	42.5	531	2	G89667	protein F17B5.2 [1
4	1030.5	42.5	587	2	T21074	hypothetical prote
5	825	34.0	479	2	T49871	peroxisomal Ca-dep
6	519	21.4	352	2	T01729	mitochondrial solu
7	477	19.7	500	2	T39385	probable mitochond
8	476	19.6	358	2	T45934	hypothetical prote
9	467.5	19.3	332	2	T47703	Ca-dependent soluc
10	450	18.6	335	2	T04273	hypothetical prote
11	448.5	18.5	330	2	S25596	Graves disease mit
12	4435	18.0	348	2	D84798	probable mitochond
13	425.5	17.6	381	2	T51158	hypothetical prote
14	423.5	17.5	326	2	S57544	probable membrane
15	422	17.4	326	2	B40141	mitochondrial solu
16	415.5	17.1	436	2	T48171	hypothetical prote
17	415.5	17.1	436	2	T01459	Bcl protein precu
18	410.5	16.9	349	2	A40141	mitochondrial solu
19	383.5	15.8	324	2	T22145	hypothetical prote
20	383.5	15.8	324	2	T05350	adenylate transloc
21	373.5	15.4	418	2	B96811	hypothetical prote
22	354	14.6	326	2	T37874	probable mitochond
23	349	14.4	357	2	S46795	hypothetical prote
24	335	13.8	308	1	S30259	ADP/ATP carrier pr
25	334.5	13.8	305	2	S68154	ADP/ATP carrier pr
26	330	13.6	313	1	XWNC	ADP/ATP carrier pr
27	328	13.5	322	2	T40526	adp/ATP translocas
28	328	13.5	382	2	S33630	ADP/ATP carrier pr
29	327	13.5	379	2	S21333	ADP/ATP carrier pr

30	325	13.4	387	2	S14876	ADP/ATP carrier pr
31	324	13.4	387	2	S16568	ADP/ATP carrier pr
32	323.5	13.4	386	2	S14874	ADP/ATP carrier pr
33	323	13.3	386	2	T09709	ADP/ATP carrier pr
34	322.5	13.3	386	2	T42011	ADP/ATP carrier pr
35	322	13.3	309	2	A24849	ADP/ATP carrier pr
36	321	13.2	379	2	T04608	ADP/ATP carrier pr
37	318	13.1	386	2	S17917	ADP/ATP carrier pr
38	314	13.0	298	1	S03894	ADP/ATP carrier pr
39	314	13.0	326	2	T25728	hypothetical prote
40	314	13.0	386	2	S21974	ADP/ATP carrier pr
41	313.5	12.9	385	1	S29852	ADP/ATP carrier pr
42	313	12.9	298	2	B43646	ADP/ATP carrier pr
43	312.5	12.9	307	2	A36582	ADP/ATP carrier pr
44	309	12.8	298	2	T24029	hypothetical prote
45	308.5	12.7	318	1	A31978	ADP/ATP carrier pr
46	308.5	12.7	650	2	T32897	hypothetical prote
47	308	12.7	298	2	S37210	ADP/ATP carrier pr
48	308	12.7	781	2	A86205	hypothetical prote
49	307	12.7	331	2	T00582	probable mitochond
50	305	12.6	377	2	S36081	probable carrier p
51	304.5	12.6	298	1	A44778	ADP/ATP carrier pr
52	303	12.5	339	2	A41677	ADP/ATP carrier pr
53	302	12.5	298	1	A29132	ADP/ATP carrier pr
54	300	12.4	298	2	I60173	adenine nucleotide
55	297	12.3	298	1	XWBO	ADP/ATP carrier pr
56	297	12.3	298	2	S31814	ADP/ATP carrier pr
57	295	12.2	301	2	S51132	ADP/ATP carrier pr
58	293	12.1	306	2	T20012	hypothetical prote
59	292.5	12.1	494	2	S57539	probable membrane
60	282	11.6	325	2	JC7553	brain mitochondria
61	281.5	11.6	371	2	T50159	probable carrier p
62	280	11.6	322	2	S57116	hypothetical prote
63	277.5	11.5	313	2	T25850	hypothetical prote
64	277.5	11.5	313	2	T23207	probable membrane
65	277.5	11.5	314	2	S64401	probable membrane
66	275	11.3	373	2	S48451	hypothetical prote
67	274	11.3	300	2	T15206	hypothetical prote
68	274	11.3	303	2	T39149	probable RNA splic
69	274	11.3	335	2	S50453	hypothetical prote
70	273.5	11.3	277	2	T40033	probable mitochond
71	272	11.2	301	1	S31935	ADP/ATP carrier pr
72	270.5	11.2	300	2	T25371	hypothetical prote
73	263	10.9	304	2	S15333	mtRNA splice defec
74	261.5	10.8	702	2	T16533	hypothetical prote
75	261	10.8	343	2	T15253	hypothetical prote
76	259	10.7	311	2	S48400	carrier protein FL
77	258	10.6	300	2	T21149	hypothetical prote
78	256.5	10.6	305	2	H86274	F7A19.22 protein -
79	254.5	10.5	357	2	G96770	hypothetical prote
80	251	10.4	314	2	S55179	mtRNA splice defec
81	249.5	10.3	314	2	T39510	probable mitochond
82	246	10.2	338	2	T40968	probable mitochond
83	242	10.2	333	2	T25459	hypothetical prote
84	240.5	9.9	902	1	S54495	probable carrier p
85	239	9.9	844	2	B84773	probable mitochond
86	237.5	9.8	351	2	T43493	hypothetical prote
87	236	9.7	302	2	T38879	uncoupling protei
88	236	9.7	312	2	JC5522	uncoupling protei
89	235	9.7	309	2	T48156	hypothetical prote
90	234.5	9.7	312	2	T26089	hypothetical prote
91	232.5	9.6	311	2	G86383	probable mitochond
92	232.5	9.6	447	2	T00435	probable mitochond
93	231	9.5	296	2	T23170	hypothetical prote
94	229	9.5	307	2	S60949	probable phosphat
95	228	9.4	327	2	T51577	ADP/ATP translocas
96	227	9.4	328	2	T19322	hypothetical prote
97	226	9.3	360	2	T19105	phosphate carrier
98	225.5	9.3	307	2	G01858	uncoupling protei
99	224.5	9.3	296	2	B96830	hypothetical prote
100	221	9.1	313	2	D84613	hypothetical prote
101	221	9.1	368	2	S54524	hypothetical prote
102	220.5	9.1	307	2	A26294	uncoupling protei

103	219.5	9.1	311	2	S12318	phosphate transpor
104	218.5	9.0	394	1	S44092	probable carrier p
105	218	9.0	306	2	T47570	uncoupling protein
106	218	9.0	309	2	T29325	hypothetical prote
107	217.5	9.0	330	2	T09382	hypothetical prote
108	214	8.8	313	2	T05577	uncoupling protein
109	213.5	8.8	307	2	S34268	uncoupling protein
110	213	8.8	314	2	A56650	2-oxoglutarate car
111	212	8.7	306	2	A32446	uncoupling protei
112	212	8.7	309	2	B84550	hypothetical prote
113	212	8.7	366	2	S64589	hypothetical prote
114	209	8.6	284	2	T18253	probable mitochon
115	209	8.6	306	2	T52024	uncoupling protei
116	209	8.6	314	2	A53305	2-oxoglutarate/mal
117	209	8.6	355	2	T09110	envelope protein l
118	208.5	8.6	311	2	A46595	tricarboxylate tra
119	207.5	8.6	358	2	T09109	envelope protein l
120	207	8.5	269	2	T20290	hypothetical prote
121	206.5	8.5	352	2	A53737	phosphate carrier
122	206	8.5	320	2	S44091	oxoglutarate/malat
123	205.5	8.5	334	2	T19278	hypothetical prote
124	205	8.5	312	2	H88567	protein KLIH3.3 [l
125	205	8.5	361	2	BS3737	phosphate carrier
126	201.5	8.3	306	2	A31106	mitochondrial unco
127	201	8.3	222	2	S60997	AKG11 protein - ye
128	200.5	8.3	231	2	T37992	probable tricarbox
129	199.5	8.2	311	2	G01789	citrate transpor
130	199	8.2	284	2	S45458	PF8 protein - Yea
131	199	8.2	306	2	T07793	uncoupling protein
132	198	8.2	288	2	S03603	uncoupling protei
133	197	8.1	347	2	T50990	hypothetical prote
134	196.5	8.1	327	2	S61660	probable membrane
135	195.5	8.1	332	2	T15755	hypothetical prote
136	195	8.0	374	2	T24162	hypothetical prote
137	194.5	8.0	366	2	A34350	phosphate transpor
138	193.5	8.0	362	2	CS3737	phosphate carrier
139	192	7.9	337	2	T24017	hypothetical prote
140	192	7.9	361	2	D53737	phosphate carrier
141	190.5	7.9	303	2	T00969	probable mitochon
142	190.5	7.9	331	2	F84823	probable peroxisom
143	189.5	7.8	366	2	T01169	phosphate transpor
144	188	7.8	336	2	T01839	hypothetical prote
145	187.5	7.7	330	2	T29640	mitochondrial carr
146	187	7.7	345	2	T37576	probable mitochon
147	186.5	7.7	282	2	T49628	probable dicarboxy
148	185.5	7.7	374	2	S40756	hypothetical prote
149	184.5	7.6	301	2	T16844	hypothetical prote
150	183.5	7.6	375	2	T05707	phosphate transpor
151	182.5	7.5	349	2	B96753	hypothetical prote
152	182	7.5	239	2	S44554	citrate transpor
153	182	7.5	307	2	S67662	hypothetical prote
154	181.5	7.5	331	2	T51899	probable 2-oxoglut
155	180.5	7.4	335	2	T50393	probable mitochon
156	180	7.4	310	2	S69050	probable membrane
157	177.5	7.3	311	2	T50326	probable mitochon
158	177.5	7.3	409	2	T24543	hypothetical prote
159	176	7.2	363	2	T49281	mitochondrial phos
160	174.5	7.2	353	2	T51393	probable mitochon
161	173	7.1	419	2	S50283	EMP47B protein - y
162	171.5	7.1	423	2	A23667	47K peroxisomal me
163	171	7.1	310	2	T20229	hypothetical prote
164	171	7.1	334	2	S25357	mitochondrial unco
165	170.5	7.0	238	2	S51351	hypothetical prote
166	170.5	7.0	307	2	S54080	carrier protein YM
167	169.5	7.0	288	2	T51595	phosphate transpor
168	168.5	7.0	271	2	S62485	probable mitochon
169	164.5	6.8	358	2	D84901	hypothetical prote
170	164	6.8	344	2	A84750	probable mitochon
171	162.5	6.7	300	2	A40803	tropomyosin C, skelet
172	162	6.7	302	2	S50556	hypothetical prote
173	161.5	6.7	163	2	JM0063	fast skeletal trop
174	160.5	6.6	162	1	TPFGCS	tropomyosin C, skelet
175	160.5	6.6	302	2	S65042	2-oxoglutarate/mal
176	159.5	6.6	176	2	JM0062	fast skeletal trop
177	159	6.6	177	2	S48269	mitochondrial carr
178	158.5	6.5	178	2	S65040	2-oxoglutarate/mal
179	157.5	6.5	179	2	T07405	oxoglutarate/malat
180	156.5	6.5	180	2	T18434	tropomyosin C isoform
181	156.5	6.5	181	2	TPCHCS	tropomyosin C, skelet
182	155.5	6.4	182	2	A38383	tropomyosin C, fast s
183	154.5	6.4	183	2	TPPGCS	tropomyosin C, skelet
184	154	6.4	184	2	T39347	probable tricarbox
185	153	6.3	185	2	JM0032	calmodulin - fungu
186	152.5	6.3	186	2	TPPRCS	tropomyosin C, fast s
187	149.5	6.2	187	2	T37603	probable oxalacet
188	148.5	6.1	188	2	T20858	hypothetical prote
189	148	6.1	189	2	JMCAS	calmodulin - Emeri
190	148	6.1	190	2	CA4216	calmodulin - Apep
191	148	6.1	191	2	S58709	calmodulin - Neuro
192	148	6.1	192	2	S38877	tropomyosin C isoform
193	148	6.1	193	2	S69019	hypothetical prote
194	147.5	6.1	194	2	TPHUCS	tropomyosin C, fast s
195	147.5	6.1	195	2	T24672	calmodulin - Chlam
196	146	6.0	196	2	MCKM	tropomyosin C - Flox
197	146	6.0	197	2	JM0061	tropomyosin C - commo
198	145	6.0	198	2	JM0060	probable carrier p
199	145.5	6.0	199	2	S58779	calcium-stimulated
200	145	6.0	200	2	S54788	tropomyosin C isoform
201	144.5	5.9	201	2	S18394	calmodulin - garde
202	144	5.9	202	2	T06437	probable calmodul
203	144	5.9	203	2	P96794	tropomyosin C isoform
204	143.5	5.9	204	2	S18435	fast skeletal trop
205	143.5	5.9	205	2	JM0065	tropomyosin C
206	143	5.9	206	2	S43240	tropomyosin C - commo
207	142	5.9	207	2	A71409	calmodulin 8 [impo
208	142	5.9	208	2	T10726	calmodulin - green
209	141.5	5.8	209	2	A34380	tropomyosin C alpha -
210	141.5	5.8	210	2	J01232	calcineurin regula
211	141.5	5.8	211	2	T24178	hypothetical prote
212	141	5.8	212	2	A32620	tropomyosin C, cardia
213	140.5	5.8	213	2	B34380	tropomyosin C gamma -
214	140.5	5.8	214	2	A40394	spec-related prote
215	140	5.8	215	2	TN0722	calmodulin - Pneum
216	140	5.8	216	1	TPBOCC	tropomyosin C, cardia
217	140	5.8	217	2	A27204	tropomyosin C, cardia
218	139	5.8	218	2	JU0035	calmodulin - soybe
219	139	5.7	219	2	T08585	calmodulin - sea
220	138	5.7	220	2	TPHUTC	tropomyosin C, cardia
221	138	5.7	221	1	TPRBCW	tropomyosin C, cardia
222	137.5	5.7	222	1	MCPO	calmodulin - potat
223	137	5.7	223	1	MCSN	calmodulin - ecall
224	137	5.7	224	1	MCSAM	calmodulin - sea a
225	137	5.7	225	2	S58314	calmodulin - moss
226	137	5.7	226	2	F86379	protein F21J9.28 [
227	136	5.6	227	1	MCWT	calmodulin - wheat
228	136	5.6	228	2	T07122	calmodulin CAM5 -
229	136	5.6	229	2	S38678	tropomyosin C isoform
230	136	5.6	230	1	BCKM	calmodulin - Chlam
231	135.5	5.6	231	2	S70767	calmodulin CAM72 -
232	135	5.6	232	1	MCTZR	calmodulin - sea p
233	135	5.6	233	2	T47240	amino acid transpo
234	134.5	5.6	234	2	T10564	hypothetical-l
235	134	5.5	235	2	T50929	calmodulin-1 [impo
236	134	5.5	236	2	JC1033	calmodulin - garde
237	134	5.5	237	1	MCKKA	calmodulin - yeast
238	134	5.5	238	2	S53006	calmodulin - leaf
239	134	5.5	239	1	S22503	calmodulin [slm1a
240	134	5.5	240	2	H84667	calmodulin (cam2)
241	134	5.5	241	2	S35187	calmodulin 6 - Ara
242	134	5.5	242	2	E96689	calmodulin import
243	134	5.5	243	2	T06644	calmodulin homolog
244	133.5	5.5	244	2	A38397	tropomyosin C-1 - gia
245	133.5	5.5	245	2	T27963	hypothetical prote
246	133.5	5.5	246	2	JC1221	calcineurin regula
247	133.5	5.5	247	2	T02895	hypothetical prote
248	133	5.5	248	2	T16039	hypothetical prote

249	133	5.5	149	2	S58311	calmodulin - Blden	322	123	5.1	530	2	A84847	probable Ca2+ depe
250	133	5.5	167	2	B85437	caltractin-like pr	323	122	5.0	149	1	MCTE	calmodulin - Tetra
251	133	5.5	169	2	T45582	centrin Arabidop	324	122	5.0	149	1	MCZOF	calmodulin - melar
252	133	5.5	297	2	T40082	mitochondrial carr	325	122	5.0	149	2	S28954	calmodulin - Tetra
253	132.5	5.5	161	2	JW0064	slow cardiac tropo	326	122	5.0	500	2	T26786	hypothetical prote
254	132.5	5.5	162	2	JW0066	slow cardiac tropo	327	121.5	5.0	150	2	T15596	hypothetical prote
255	132.5	5.5	317	1	A31797	Spec-related prote	328	121.5	5.0	170	1	AC3391	calcineurin regula
256	132.5	5.5	560	2	T46189	calcium-dependent	329	121.5	5.0	170	1	JC1320	calcineurin regula
257	132	5.4	148	1	MCA2S	calmodulin - sea	330	121.5	5.0	170	1	S34127	calcineurin regula
258	132	5.4	149	2	S60237	calmodulin PCW2/PC	331	121.5	5.0	216	1	S42716	calcineurin regula
259	132	5.4	149	2	S22860	calmodulin 2 (clon	332	121.5	5.0	221	2	T25027	hypothetical prote
260	132	5.4	149	2	S51933	calmodulin cam2 -	333	121.5	5.0	359	2	T22708	hypothetical prote
261	132	5.4	165	2	PS0261	calcineurin regula	334	121	5.0	153	2	S45681	troponin C - scal1
262	131	5.4	142	2	T06791	calmodulin TacAm2-	335	121	5.0	161	2	S42551	caltractin - Scher
263	131	5.4	148	1	MCSP	calmodulin - spina	336	120.5	5.0	161	2	T42006	troponin C - Caeno
264	131	5.4	148	2	JC1094	calmodulin - rice	337	120.5	5.0	169	2	D84864	probable calcium b
265	131	5.4	149	1	MCA	calmodulin - alfai	338	120	5.0	187	2	T02887	probable calmoduli
266	131	5.4	149	1	MCBH	calmodulin - barley	339	117.5	4.8	204	2	A57604	guanylate cyclase-
267	131	5.4	149	1	MCCHM	calmodulin - striat	340	119.5	4.9	149	2	A33353	calcium-binding pr
268	131	5.4	149	1	MCPZDC	calmodulin - carro	341	118.5	4.8	300	2	T41066	mitochondrial carr
269	131	5.4	149	1	S22971	calmodulin - trump	342	117.5	4.8	151	2	B38397	troponin C-2- gia
270	131	5.4	149	1	S40301	calmodulin - red b	343	117.5	4.8	226	2	T08923	calcineurin B-like
271	131	5.4	149	1	S70768	calmodulin CAM81 -	344	116	4.8	152	2	A53051	troponin C (Ca(2+)
272	131	5.4	149	2	S24952	calmodulin 1 (clon	345	116	4.8	157	2	D96689	calmodulin-related
273	131	5.4	149	2	T47417	calmodulin 7 (elml	346	116	4.8	170	2	JC7242	calcineurin regula
274	130	5.4	150	2	S35185	calmodulin 4 - Ara	347	115.5	4.8	191	2	A48979	visinin-like prote
275	130	5.4	150	1	MCZP	calmodulin - fib81	348	115.5	4.8	191	2	JH0605	neural visinin-lik
276	130	5.4	151	1	MCD	calmodulin - slime	349	115	4.7	187	2	A84532	probable calmoduli
277	130	5.4	161	2	S07450	troponin C - quail	350	115	4.7	258	2	T19401	hypothetical prote
278	130	5.4	316	2	T49376	hypothetical prote	351	115	4.7	513	1	T02259	calcium-dependent
279	129	5.3	131	2	A29422	calmodulin-like pr	352	114.5	4.7	158	2	JC5434	larva muscle tropo
280	129	5.3	149	1	MCHNB	calmodulin-related	353	114	4.7	149	1	MCTIMAK	calmodulin - Achly
281	129	5.3	149	2	S51932	calmodulin cam1 -	354	114	4.7	524	2	A45472	protein kinase (EC
282	128	5.3	153	2	UX0072	troponin C, striat	355	113.5	4.7	170	2	A44307	calcineurin regula
283	128.5	5.3	178	2	S56300	hypothetical prote	356	113.5	4.7	195	2	JC5174	calcineurin regula
284	128	5.3	141	2	S02680	calmodulin A - sea	357	113.5	4.7	182	2	T49012	calmodulin-like pr
285	128	5.3	148	1	MCON	calmodulin - salmo	358	113	4.7	182	2	S71318	centrin ICL1b - Pa
286	128	5.3	148	1	MCBO	calmodulin [valida	359	113	4.7	183	2	S71319	centrin ICL1c - Pa
287	128	5.3	148	1	MCSFCU	calmodulin - sea c	360	113	4.7	465	1	T03024	calcium-dependent
288	128	5.3	149	1	IS1202	calmodulin - duck	361	113	4.7	520	2	F85059	probable calcium d
289	128	5.3	149	1	MCH	calmodulin - chick	362	112.5	4.6	164	2	T29903	hypothetical prote
290	128	5.3	149	1	MCEE	calmodulin - elect	363	112.5	4.6	197	2	AB2713	cytosol aminopepti
291	128	5.3	149	1	MCHU	calmodulin [valida	364	112.5	4.6	522	2	B97495	cytosol aminopepti
292	128	5.3	149	1	MCHT	calmodulin [valida	365	112	4.6	181	2	S71317	centrin ICL1a - Pa
293	128	5.3	149	1	MCUTC	calmodulin - Trypa	366	111.5	4.6	147	1	MGBY	calmodulin - yeast
294	128	5.3	149	1	MCUTG	calmodulin - Trypa	367	111.5	4.6	158	2	JC5433	adult muscle tropo
295	128	5.3	149	2	JC1305	calmodulin - Japan	368	111.5	4.6	490	1	S71776	calcium-dependent
296	128	5.3	149	2	IS1402	calmodulin - Afric	369	111.5	4.6	610	1	A49082	calmodulin homolog
297	128	5.3	149	2	S37707	calmodulin - mouse	370	111	4.6	90	2	A44977	calmodulin homolog
298	128	5.3	149	2	T49567	calmodulin - mouse	371	111	4.6	172	2	S38531	caltractin - mouse
299	128	5.3	149	2	A48111	calmodulin C - Try	372	111	4.6	293	2	T40702	mitochondrial carr
300	127	5.2	148	2	S02691	calmodulin B - sea	373	111	4.6	503	2	T51156	calcium dependent
301	127	5.2	148	1	MCEG	calmodulin - Eugle	374	110.5	4.6	191	2	JH0815	neural visinin-lik
302	127	5.2	148	1	MCLQ	calmodulin - migra	375	110.5	4.6	196	2	T51357	calcium-dependent
303	127	5.2	148	1	MCMRP	calmodulin - cornu	376	110.5	4.6	226	2	T51357	calcineurin B-like
304	127	5.2	149	1	MCPR	calmodulin [valida	377	110	4.5	170	2	A86317	protein T10022.19
305	127	5.2	149	1	MCGAC	calmodulin - Calif	378	109.5	4.5	174	2	T41632	probable calcineur
306	127	5.2	149	1	MCP	calmodulin - Param	379	109.5	4.5	190	2	T51686	freiquenln - Africa
307	127	5.2	149	1	T31737	hypothetical prote	380	109.5	4.5	553	1	T02139	calcium-dependent
308	126	5.2	573	2	T09940	calcium-dependent	381	109.5	4.5	1146	2	B70376	reverse gyrase - A
309	125.5	5.2	154	2	G85041	probable calmoduli	382	109	4.5	151	2	T49071	probable calmoduli
310	125	5.2	124	2	S60235	calmodulin PCW3 -	383	109	4.5	311	2	T42088	hypothetical prote
311	125	5.2	149	2	S40086	calmodulin calml -	384	108.5	4.5	385	2	F86464	hypothetical prote
312	125	5.2	169	2	T10724	probable caltracti	385	108.5	4.5	727	2	A56879	diacylglycerol kin
313	125	5.2	298	2	A28260	chromosomal protei	386	108	4.5	178	2	S44624	CSOC3.5 protein -
314	124	5.1	371	2	T18568	probable microchond	387	107.5	4.4	514	2	T10938	calcium-dependent
315	123.5	5.1	150	2	H86194	hypothetical prote	388	107	4.4	165	2	A44103	neurocalcin beta -
316	123.5	5.1	161	2	A24921	calmodulin-like pr	389	107	4.4	224	2	F96668	protecin PIN19.5 [i
317	123.5	5.1	218	2	T19229	hypothetical prote	390	107	4.4	540	1	T01989	calcium-dependent
318	123.5	5.1	334	2	T02109	calmodulin-like pr	391	107	4.4	563	2	H84810	probable calcium-d
319	123	5.1	148	1	MCRB	calmodulin - rabbi	392	107	4.4	862	1	FAD0AA	alpha-actinin - bl
320	123	5.1	149	2	JC1309	calmodulin - Stylo	393	106.5	4.4	155	2	A28853	troponin C, smooth
321	123	5.1	149	2	S53019	calmodulin - Macro	394	106.5	4.4	205	2	T08398	calmodulin homolog

395	106.5	4.4	270	2	JC7631	K+ channel-interac	468	97.5	4.0	246	2	T05308	hypothetical prote
396	106.5	4.4	425	2	S17759	protein kinase, ca	469	97.5	4.0	246	2	H85387	hypothetical prote
397	106.5	4.4	532	2	T14335	protein kinase, ca	470	97.5	4.0	336	2	JC4102	hypothetical 36.9k
398	106.5	4.4	554	2	T05476	calcium-dependent	471	97.5	4.0	830	2	F83659	stage II sporulat
399	106	4.4	172	2	A49652	caltractin - human	472	97.5	4.0	1031	1	A38713	kinesin heavy chal
400	106	4.4	190	2	S61168	hypothetical prote	473	97.5	4.0	189	2	A49020	calcium-binding pr
401	106	4.4	214	2	T08922	hypothetical prote	474	97	4.0	190	2	S58303	related to neurona
402	106	4.4	536	2	T05500	calcium-dependent	475	97	4.0	193	2	JH0816	neural vistin-11k
403	105.5	4.4	198	2	S68839	guanylate cyclase-	476	97	4.0	571	2	A81797	hypothetical prote
404	105	4.3	495	1	S46284	calcium-dependent	477	97	4.0	975	2	A86258	protein F5011.4 [l
405	105	4.3	639	1	T02784	calcium-dependent	478	97	4.0	1302	2	A41249	multidrug resistan
406	105	4.3	2477	1	SJCH4	spectrin alpha cha	479	97	4.0	2472	2	A35715	fodrin alpha chain
407	104.5	4.3	521	2	G96543	calcium-dependent	480	96.5	4.0	195	2	JC1347	hippocalcin - rat
408	104.5	4.3	531	2	D85059	probable calcium d	481	96.5	4.0	629	2	A56536	plastin, intestina
409	104.5	4.3	533	1	S56522	calcium-dependent	482	96.5	4.0	700	2	B81266	DNA topoisomerase
410	104	4.3	174	2	T47245	calcineurin regula	483	96.5	4.0	1036	2	A82357	probable multidrug
411	104	4.3	177	2	G96794	probable calmoduli	484	96	4.0	157	2	A82357	hypothetical prote
412	104	4.3	263	2	A34466	calpain (EC 3.4.22	485	96	4.0	184	2	A53143	calpain (EC 3.4.22
413	104	4.3	575	2	G85059	calpain (EC 3.4.22	486	96	4.0	193	2	JH0616	neurocalcin (clone
414	104	4.3	810	1	S57196	calpain (EC 3.4.22	487	96	4.0	268	1	C1H0L	calpain (EC 3.4.22
415	103.5	4.3	153	2	S04970	calcium-binding pr	488	96	4.0	484	2	T05650	calcium-dependent
416	103.5	4.3	201	2	C55331	guanylate cyclase	489	96	4.0	541	2	P96776	hypothetical prote
417	103.5	4.3	633	2	C32571	ribosomal protein	490	96	4.0	704	2	T03478	probable DNA-dirc
418	103.5	4.3	740	2	I38556	centrin - human	491	96	4.0	862	2	T29133	hypothetical prote
419	103	4.3	172	2	I38424	hypothetical prote	492	95.5	3.9	193	2	S47565	calcium-binding pr
420	103	4.3	254	2	T29566	hypothetical prote	493	95.5	3.9	778	2	D74241	xylosidase - Therm
421	103	4.3	314	2	S56055	RNA polymerase sig	494	95.5	3.9	795	1	D64226	endopeptidase Ia (
422	103	4.3	378	2	D97060	transcription init	495	95.5	3.9	1101	2	T33153	hypothetical prote
423	103	4.3	378	2	I40610	hypothetical prote	496	95	3.9	166	2	A86447	hypothetical prote
424	102.5	4.2	264	2	T34330	protein calmodulin	497	95	3.9	198	2	A25706	'boerin - Chinese h
425	102	4.2	163	2	G96763	protein calmodulin	498	95	3.9	237	2	T16357	hypothetical prote
426	102	4.2	198	2	S52094	scorcin - human	499	95	3.9	318	2	I56519	calpoxin-associate
427	102	4.2	529	1	S71774	calcium-dependent	500	95	3.9	407	2	S53353	calflagin Tb-44A
428	101.5	4.2	508	2	A43713	calcium-dependent	501	95	3.9	575	2	S77416	succinate dehydrog
429	101.5	4.2	902	2	T49878	respiratory burst	502	94.5	3.9	142	2	T24862	hypothetical prote
430	101.5	4.2	3455	2	B82519	hemagglutinin-like	503	94.5	3.9	271	1	S25006	calactinin - rat
431	101	4.2	200	2	JC1227	recoverin - human	504	94.5	3.9	640	2	P90364	hypothetical prote
432	101	4.2	211	1	A34311	flagellar calcium-	505	94	3.9	80	2	A45940	calmodulin - sea u
433	101	4.2	262	1	KLCHI	calcium-binding pr	506	94	3.9	168	2	S62881	calcium binding pr
434	101	4.2	575	2	AC2177	succinate dehydrog	507	94	3.9	190	2	A55666	neurocalcin - fru
435	101	4.2	823	2	H72282	maltoase ABC transp	508	94	3.9	269	1	A27067	calactinin - chick
436	100.5	4.1	404	2	T19445	hypothetical prote	509	94	3.9	317	2	I37371	ER calcium-binding
437	100.5	4.1	531	1	T02093	calcium-dependent	510	94	3.9	342	2	B70889	hypothetical prote
438	100.5	4.1	745	1	T02024	cytochrome b245 be	511	94	3.9	368	2	S40627	hypothetical prote
439	100	4.1	149	2	S64114	hypothetical prote	512	94	3.9	382	2	JC7811	calcyphosine 2, EF
440	100	4.1	202	2	B55331	guanylate cyclase-	513	93.5	3.9	150	1	MOCHA2	myosin alkali ligh
441	100	4.1	266	1	C1PGL	calpain (EC 3.4.22	514	93.5	3.9	189	2	T20411	hypothetical prote
442	100	4.1	543	2	D64243	heat shock protein	515	93.5	3.9	192	1	MOCHLA	myosin alkali ligh
443	99.5	4.1	175	2	JH0462	phosphoprotein pho	516	93.5	3.9	205	2	S46233	allergen Bec v III
444	99.5	4.1	213	2	T51356	calcineurin B-like	517	93.5	3.9	578	2	A64696	hypothetical prote
445	99.5	4.1	229	2	T15359	hypothetical prote	518	93.5	3.9	695	2	T52429	PRM1 homolog (po
446	99.5	4.1	544	2	T08873	calcium-dependent	519	93.5	3.9	733	2	A57459	ribosomal protein
447	99.5	4.1	540	2	D84550	probable calmoduli	520	93.5	3.9	2183	1	Z1ZNMV	genome polypeptin
448	99.5	4.1	937	2	T40723	c-I-tetrahydrofola	521	93	3.8	189	2	S03635	calcyphosine - dog
449	99	4.1	266	1	C1RBL	calpain (EC 3.4.22	522	93	3.8	193	2	I50676	gene Rem-1 protein
450	99	4.1	501	2	G85097	hypothetical prote	523	93	3.8	188	2	S14665	probable calcium-b
451	99	4.1	537	2	H87502	conserved hypotet	524	93	3.8	199	2	S68838	guanylate cyclase-
452	98.5	4.1	193	2	JC2186	hippocalcin - huma	525	93	3.8	233	1	AQUH17	flagellar calcium-
453	98.5	4.1	365	2	C64421	hypothetical prote	526	93	3.8	339	2	S74048	probable denonubi
454	98.5	4.1	356	2	T06126	calcium-dependent	527	93	3.8	399	2	C71728	probable oxygen-in
455	98	4.0	147	2	A29910	myosin calcium-bin	528	93	3.8	583	1	H71326	probable protein-e
456	98	4.0	151	1	KLBOB	Specic protein - s	529	93	3.8	734	1	S09156	diacylglycerol kin
457	98	4.0	260	1	MCUR2C	calcium-binding pr	530	93	3.8	764	1	S14113	1-phosphatidylol
458	98	4.0	261	1	A34955	calcium-binding pr	531	93	3.8	2415	1	A33733	spectrin alpha cha
459	98	4.0	261	1	KLRTB	calcium-binding pr	532	92.5	3.8	194	1	MOCHLC	myosin alkali ligh
460	98	4.0	261	1	S00234	calcium-binding pr	533	92.5	3.8	554	2	AH2651	ABC transporter, m
461	98	4.0	368	2	G83180	probable FMN oxido	534	92.5	3.8	571	2	G97433	iron (III) ABC tran
462	98	4.0	484	2	B72048	ABC transporter -	535	92.5	3.8	571	2	T00835	calcium-dependent
463	98	4.0	484	2	A86577	ABC transporter [i	536	92.5	3.8	684	2	G90473	hypothetical prote
464	98	4.0	516	2	H87369	tryptophan halogen	537	92.5	3.8	859	2	B85718	probable tail comp
465	97.5	4.0	146	2	F84777	probable calmoduli	538	92.5	3.8	862	1	ORMSLD	LDL receptor precu
466	97.5	4.0	191	2	S35188	calcium binding pr	539	92.5	3.8	1134	2	D75014	hypothetical prote
467	97.5	4.0	192	2	T01375	calcium sensor hom	540	92	3.8	344	2	D90325	alcohol dehydrogen

541	92	3.8	429	2	AG3150	hypothetical prote	614	89	3.7	403	2	T44836	glycoyltransferas
542	92	3.8	540	2	T15573	hypothetical prote	615	89	3.7	461	2	F90568	hypothetical prote
543	92	3.8	608	2	T18445	hypothetical prote	616	89	3.7	533	1	S7178	calcium-dependent
544	92	3.8	631	2	B98137	hypothetical 46.1K	617	89	3.7	543	2	UC4991	detergent sensitiv
545	92	3.8	805	1	A55054	calpain (EC 3.4.22	618	89	3.7	614	2	D87410	loid protein (limpo
546	92	3.8	842	2	E72373	hypothetical prote	619	89	3.7	787	2	A81940	probable phenylala
547	92	3.8	1050	2	S45636	natriuretic-peptid	620	89	3.7	2413	2	S34670	splicing factor PR
548	92	3.8	1817	2	AD2165	two-component hybr	621	89	3.7	4687	1	A39638	plectin - rat
549	91.5	3.8	150	1	MCUR2A	Spec 2a protein -	622	89	3.7	4967	2	S72259	ryanodine receptor
550	91.5	3.8	161	2	A29357	calcium-binding pr	623	89	3.7	83	2	TS1474	calcium-binding pr
551	91.5	3.8	162	2	UC7157	calcium vector pro	624	88.5	3.7	166	2	T07949	calcium-binding pr
552	91.5	3.8	319	2	UC5402	vitamin D receptor	625	88.5	3.7	356	2	D85827	histidinol-phospha
553	91.5	3.8	374	2	D72319	flagellar biosynth	626	88.5	3.7	356	2	F90981	histidinol-phospha
554	91.5	3.8	590	1	TYEFP5	protein-tyrosine k	627	88.5	3.7	387	2	AE2253	hypothetical prote
555	91.5	3.8	636	2	A48872	dnak-type molecula	628	88.5	3.7	443	2	C72394	hypothetical prote
556	91.5	3.8	640	2	S37394	dnak-type molecula	629	88.5	3.7	418	2	A11780	probable phosphos
557	91.5	3.8	667	2	T35491	probable serine/th	630	88.5	3.7	446	2	T36828	probable transcrip
558	91.5	3.8	879	1	ORRTUD	LDL receptor precu	631	88.5	3.7	451	2	S56717	calcium-dependent
559	91.5	3.8	2541	2	T29340	hypothetical prote	632	88.5	3.7	470	1	C64525	mannose-6-phosphat
560	91	3.8	69	2	A30792	calcium-binding pr	633	88.5	3.7	538	2	T08874	calcium-dependent
561	91	3.8	191	2	T10520	probable calcium-b	634	88.5	3.7	557	2	AE2609	exodeoxyribonuclea
562	91	3.8	475	2	UN0578	p-Aminobenzoic aci	635	88.5	3.7	557	2	D97391	xsea, exodeoxyribo
563	91	3.8	498	2	T04640	hypothetical prote	636	88.5	3.7	892	2	F64703	DNA polymerase I -
564	91	3.8	1906	2	AD2443	hypothetical prote	637	88.5	3.7	1233	2	IS4383	chromosome segrega
565	91	3.8	26926	1	I38344	hypothetical prote	638	88.5	3.7	1290	2	A31317	1-phosphatidylinos
566	90.5	3.7	193	1	MOM54E	ctitin, cardiac mus	639	88.5	3.7	2019	2	T27702	hypothetical prote
567	90.5	3.7	421	2	TS0138	myosin alkali ligh	640	88.5	3.7	4588	2	T28667	hypothetical prote
568	90.5	3.7	467	2	D72461	hypothetical prote	641	88	3.6	161	2	A30938	dynein beta heavy
569	90.5	3.7	487	1	S71770	hypothetical prote	642	88	3.6	218	2	S53354	myosin regulatory
570	90.5	3.7	647	2	T45522	calcium-dependent	643	88	3.6	229	2	S53355	calflagin TP-24 -
571	90.5	3.7	735	2	S12969	heat shock protein	644	88	3.6	311	2	E98240	calflagin TP-1.7 -
572	90.5	3.7	835	2	T26086	diacylglycerol kin	645	88	3.6	344	2	AG3045	ABC transporter ho
573	90.5	3.7	859	2	B90758	hypothetical prote	646	88	3.6	344	2	T12263	dioxynase (limpor
574	90.5	3.7	950	2	A82966	probable tail leng	647	88	3.6	435	2	C95975	NADH2 dehydrogenas
575	90.5	3.7	962	1	S57342	adenylate cyclase	648	88	3.6	443	2	D69306	probable polyacch
576	90.5	3.7	1070	2	T06733	endopeptidase Ia h	649	88	3.6	458	2	E81112	conserved hypothet
577	90.5	3.7	1085	2	T18559	kinesin homolog F2	650	88	3.6	464	2	C84782	UDP-N-acetylmurama
578	90	3.7	146	2	TS1473	calmodulin-like pr	651	88	3.6	485	2	AG3409	probable pyruvate
579	90	3.7	151	2	B26092	myosin I2 catalyti	652	88	3.6	521	2	T34583	leucyl aminopeptid
580	90	3.7	202	2	S21155	recoverin - mouse	653	88	3.6	600	2	T01062	probable periplasm
581	90	3.7	244	2	B84025	hypothetical prote	654	88	3.6	638	2	AB0446	hypothetical prote
582	90	3.7	364	2	T33474	hypothetical prote	655	88	3.6	715	2	B83518	probable exported
583	90	3.7	374	2	A42264	membrane-associate	656	88	3.6	783	2	AH2226	pimeoyl-CoA synth
584	90	3.7	472	2	B37777	hypothetical prote	657	88	3.6	821	1	AH2226	hypothetical prote
585	90	3.7	491	2	T45236	methyl viologene-re	658	88	3.6	837	1	A29512	calpain (EC 3.4.22
586	90	3.7	500	2	T20869	probable membrane	659	88	3.6	848	2	AD0064	LDL receptor precu
587	90	3.7	572	1	D64247	hypothetical prote	660	88	3.6	968	2	C82712	ATP-dependent seri
588	90	3.7	646	2	B86295	phosphotransferase	661	88	3.6	1010	2	F75134	RNA polymerase as
589	90	3.7	651	2	T45517	hypothetical prote	662	88	3.6	1466	2	S65741	hypothetical prote
590	90	3.7	652	2	H71494	heat shock protein	663	87.5	3.6	187	1	MORH4E	1-phosphatidylinos
591	90	3.7	1434	2	C82923	probable thiol-dis	664	87.5	3.6	208	1	MOHUSA	myosin alkali ligh
592	90	3.7	1705	2	S51672	DNA-directed RNA p	665	87.5	3.6	345	2	T09018	myosin alkali ligh
593	90	3.7	1788	2	T29043	adenylate cyclase	666	87.5	3.6	397	2	D71413	probable calcium-b
594	90	3.7	3225	2	D81702	hypothetical prote	667	87.5	3.6	448	2	A13040	hypothetical prote
595	89.5	3.7	193	1	MORT4E	adherence factor T	668	87.5	3.6	460	2	C98245	hydroxylase (limpor
596	89.5	3.7	273	2	AG1470	myosin alkali ligh	669	87.5	3.6	460	2	C98245	sdeb gene homolog
597	89.5	3.7	335	2	A45805	conserved hypotet	670	87.5	3.6	503	1	UC4999	ITP dehydrogenase
598	89.5	3.7	539	2	F85036	dnak-type molecula	671	87.5	3.6	522	2	B72589	hypothetical prote
599	89.5	3.7	551	2	A83889	hypothetical prote	672	87.5	3.6	555	2	B81859	phospholipase D-fam
600	89.5	3.7	642	2	T45298	hypothetical prote	673	87.5	3.6	588	2	D72062	single-stranded-DN
601	89.5	3.7	644	2	A45635	dnak-type molecula	674	87.5	3.6	588	2	G86560	dnak-type molecula
602	89.5	3.7	653	2	A42582	dnak-type molecula	675	87.5	3.6	593	2	G86536	cadmium efflux ATP
603	89.5	3.7	713	2	AC3220	dnak-type molecula	676	87.5	3.6	775	2	C95921	hypothetical prote
604	89.5	3.7	755	2	B95302	catallase C (import	677	87.5	3.6	877	2	T03098	hypothetical prote
605	89.5	3.7	775	2	T46719	Fix12 El-B2 type c	678	87.5	3.6	1272	2	C90593	p37 protein - Toxo
606	89.5	3.7	854	1	ORHYLD	probable vacuolar	679	87.5	3.6	1693	2	S76086	beta transducin-1i
607	89.5	3.7	1026	2	AB0771	LDL receptor precu	680	87.5	3.6	3394	2	T18501	hypothetical prote
608	89	3.7	93	2	S16082	probable RND-famil	681	87	3.6	176	2	T41061	EF-hand calcium bi
609	89	3.7	161	2	T23300	uncoupling protein	682	87	3.6	311	2	T21563	hypothetical prote
610	89	3.7	202	2	A46129	hypothetical prote	683	87	3.6	327	2	A85165	hypothetical prote
611	89	3.7	333	2	A84523	recoverin - bovine	684	87	3.6	376	2	T48950	cysteine proteinas
612	89	3.7	386	2	D59237	probable steroid s	685	87	3.6	395	2	G90565	restriction modifi
613	89	3.7	388	2	H64427	probable citrate s	686	87	3.6	460	2	F83953	hypothetical prote
						hypothetical prote				463	2	T02653	avirPct2-induced pr

687	87	3.6	470	2	D90895	probable aldehyde	760	85.5	3.5	484	2	T00716	L-allo-threonine a
688	87	3.6	470	2	D85722	probable aldehyde	761	85.5	3.5	488	2	T47787	hypothetical prote
689	87	3.6	526	2	D72107	oligopeptide bindi	762	85.5	3.5	657	2	E72486	hypothetical prote
690	87	3.6	526	2	F86515	oligopeptide bindi	763	85.5	3.5	662	2	H86723	methionine-tRNA 11
691	87	3.6	528	2	A81564	peptide ABC transp	764	85.5	3.5	672	2	T43716	dnak-type molecula
692	87	3.6	585	2	AC3422	gamma-glutamyltran	765	85.5	3.5	675	2	G71640	NADH2 dehydrogenas
693	87	3.6	733	2	A36481	myosin homolog, br	766	85.5	3.5	797	1	A99239	phosphoenolpyruvat
694	87	3.6	733	2	T22813	hypothetical prote	767	85.5	3.5	937	1	S42366	endopeptidase Ia h
695	87	3.6	739	1	VH1W6B	nucleoscapid prote	768	85.5	3.5	955	1	A35284	leukotoxin A - Pas
696	87	3.6	796	2	JC7966	xylan 1,4-beta-xyl	769	85.5	3.5	1520	2	T30820	carboxyl-phosphat
697	87	3.6	821	1	B34488	calpain (EC 3.4.22	770	85.5	3.5	2163	2	S50675	pre-mRNA splicing
698	87	3.6	839	2	SI2319	pre-mRNA splicing	771	85.5	3.5	2188	2	A70984	probable polyketid
699	87	3.6	969	2	H82068	RNA polymerase-ass	772	85.5	3.5	2427	2	T16613	hypothetical prote
700	87	3.6	1450	2	C86880	hypothetical prote	773	85.5	3.5	2478	2	T31679	bactiracin synthet
701	87	3.6	1679	2	S48385	hypothetical prote	774	85	3.5	6359	2	A56785	calmodulin - pig (
702	87	3.6	1706	1	OYBRC	cyclolysin - Borde	775	85	3.5	111	2	T07751	calmodulin 2 - tom
703	87	3.6	5627	2	C83339	hypothetical prote	776	85	3.5	237	2	AD3125	transcription regu
704	86.5	3.6	79	2	S65149	pollen allergen Br	777	85	3.5	237	2	E98162	transcription regu
705	86.5	3.6	79	2	S65151	pollen allergen Br	778	85	3.5	246	2	G90039	hypothetical prote
706	86.5	3.6	80	2	S65143	pollen allergen gr	779	85	3.5	286	2	B72404	glycine-tRNA ligas
707	86.5	3.6	82	2	S65150	pollen allergen Br	780	85	3.5	295	2	D82341	ribosomal protein
708	86.5	3.6	83	2	S65152	pollen allergen Br	781	85	3.5	314	2	AC2878	aromatic compounds
709	86.5	3.6	150	2	S01770	Specia protein - s	782	85	3.5	325	2	E97654	ABC transporter ho
710	86.5	3.6	325	2	A45337	reticulocalbin pre	783	85	3.5	336	2	G84964	glyceraldehyde-3-p
711	86.5	3.6	356	1	XNECHC	histidinol-phospha	784	85	3.5	343	2	B82418	L-allo-threonine a
712	86.5	3.6	360	2	G64575	conserved hypochet	785	85	3.5	344	2	T12252	NADH2 dehydrogenas
713	86.5	3.6	421	2	H90239	anthranilate synth	786	85	3.5	408	2	B90517	conserved hypochet
714	86.5	3.6	471	2	S78597	argininosuccinate	787	85	3.5	416	2	G86232	cysteine proteinas
715	86.5	3.6	479	2	AE2117	hypothetical prote	788	85	3.5	431	2	A72277	amidophosphoribosy
716	86.5	3.6	522	2	T39281	ars binding protei	789	85	3.5	433	2	T06407	monodehydroascorba
717	86.5	3.6	540	2	A43509	65k antigen mbaa -	790	85	3.5	491	2	E97159	genetal secretion
718	86.5	3.6	540	2	A26950	groEL2 protein - M	791	85	3.5	500	2	F84026	cytosolic axial fi
719	86.5	3.6	593	2	A64075	DNA primase (EC 2.	792	85	3.5	508	2	B81083	cardiolipin synthe
720	86.5	3.6	594	2	E83847	two-component sens	793	85	3.5	571	2	T12773	conserved hypochet
721	86.5	3.6	633	2	F88478	protein F47D12.5 (794	85	3.5	676	2	A96722	unknown protein T1
722	86.5	3.6	707	2	T42239	probable phosphopr	795	85	3.5	745	2	D96829	homeobox protein (
723	86.5	3.6	722	2	T34072	hypothetical prote	796	85	3.5	747	2	S71478	homeotic protein A
724	86.5	3.6	849	2	T41085	probable ubiquitin	797	85	3.5	765	2	H84247	adaptive-response
725	86.5	3.6	897	2	F71816	DNA polymerase I -	798	85	3.5	803	2	B56277	DNA-directed DNA p
726	86.5	3.6	1318	1	HI8BD7	internal virion pr	799	85	3.5	852	2	G87304	hypothetical prote
727	86.5	3.6	1384	1	A59289	myr 6, unconventio	800	85	3.5	878	2	H87315	hypothetical prote
728	86.5	3.6	3224	1	S58884	Ran-binding protei	801	85	3.5	889	2	AD2215	two-component hybr
729	86	3.5	69	2	JC1310	calmodulin-related	802	85	3.5	1008	1	H72310	conserved hypochet
730	86	3.5	85	2	UC5711	pollen allergen Be	803	85	3.5	1128	1	DNBEM1	DNA-binding protei
731	86	3.5	85	2	S45819	BETV4 protein - Eu	804	85	3.5	1220	2	A56236	probable RNA helic
732	86	3.5	142	2	D86348	F24B.15 protein (805	85	3.5	1574	1	A38454	myosin MYO2 - Yeas
733	86	3.5	190	2	S41476	calretinin - mouse	806	85	3.5	1603	1	V7KX5	vitellogenin vit-5
734	86	3.5	213	2	T31775	hypothetical prote	807	85	3.5	1717	2	T50247	probable helicase
735	86	3.5	331	2	JC4173	reticulocalbin pre	808	85	3.5	8243	2	T31307	type I fatty acid
736	86	3.5	332	2	B47017	probable transcrip	809	84.5	3.5	152	1	MCUR1C	Speci protein - se
737	86	3.5	332	2	AD2541	transcription init	810	84.5	3.5	195	1	MOHU3V	myosin alkali ligh
738	86	3.5	377	2	G85975	hypothetical prote	811	84.5	3.5	310	2	C95950	conserved hypochet
739	86	3.5	384	2	G91130	N-acetylglactosam	812	84.5	3.5	392	2	B81199	cell division prot
740	86	3.5	438	2	T37786	probable RNA-bindi	813	84.5	3.5	468	2	A75145	protein translocas
741	86	3.5	493	1	S46283	calcium-dependent	814	84.5	3.5	537	2	AH1277	probable transport
742	86	3.5	510	2	I38489	onconcentral ventral	815	84.5	3.5	537	2	AH1640	probable transport
743	86	3.5	530	2	T19365	hypothetical prote	816	84.5	3.5	542	1	S56651	calcium-dependent
744	86	3.5	545	2	H86322	calcium-dependent	817	84.5	3.5	582	2	E84721	probable calcium-d
745	86	3.5	558	2	T17224	hypothetical prote	818	84.5	3.5	603	2	T00379	KIA0640 protein -
746	86	3.5	803	2	B84931	DNA topoisomerase	819	84.5	3.5	630	1	A34789	T-plaestin - human
747	86	3.5	846	2	C75333	general secretion	820	84.5	3.5	666	2	F71310	probable periplasm
748	86	3.5	1139	1	PABVBS	alpha-a protein -	821	84.5	3.5	733	1	B30001	ribosomal protein
749	86	3.5	1590	2	H86398	proteina T7N9.24 [1	822	84.5	3.5	754	2	C81326	5-methyltetrahydro
750	86	3.5	1702	2	S42459	DNA-directed DNA p	823	84.5	3.5	881	2	E90997	hypothetical prote
751	86	3.5	4930	2	E66679	polyketide synthet	824	84.5	3.5	881	2	S37895	LHSL protein precu
752	85.5	3.5	190	2	T20725	hypothetical prote	825	84.5	3.5	898	2	A82298	translation initia
753	85.5	3.5	200	1	MORT3V	myosin alkali ligh	826	84.5	3.5	1093	2	S66717	hypothetical prote
754	85.5	3.5	310	1	S37695	calcium-binding pr	827	84.5	3.5	1161	2	G81186	conserved hypochet
755	85.5	3.5	327	2	D90530	hypothetical prote	828	84.5	3.5	1216	2	JM0105	synapdojanin 2 alp
756	85.5	3.5	372	2	SI8953	fix23-1 protein -	829	84.5	3.5	1367	2	T43334	chromodomain helic
757	85.5	3.5	396	2	D98103	acetate kinase (EC	830	84.5	3.5	1908	2	A86311	protein FIL3.14 [1
758	85.5	3.5	396	2	D95239	acetate kinase [lm	831	84.5	3.5	2829	2	A42271	reticulocyte-bind1
759	85.5	3.5	421	2	JC5323	anthranilate synth	832	84	3.5	143	2	T38484	calmodulin - f1s81

833	84	3.5	156	2	D90576	50S ribosomal prot	906	83	3.4	1004	2	G87323	hypothetical prote
834	84	3.5	335	2	T51489	hypothetical prote	907	83	3.4	1041	2	C85189	disease resistance
835	84	3.5	349	2	B82487	hypothetical prote	908	83	3.4	1133	2	T30302	P-type ATPase - Te
836	84	3.5	403	2	A71484	probable phosphogl	909	83	3.4	1260	2	T20487	hypothetical prote
837	84	3.5	414	2	F64386	hypothetical prote	910	83	3.4	2252	2	S06188	genome polyprotein
838	84	3.5	416	2	F98095	diaminopimelate de	911	82.5	3.4	1151	1	MOHU6N	myosin alkali ligh
839	84	3.5	426	2	F75567	serine hydroxymeth	912	82.5	3.4	151	1	MOHU6N	myosin alkali ligh
840	84	3.5	502	2	C97640	probable ATP-depen	913	82.5	3.4	151	2	S13671	non-muscle myosin
841	84	3.5	502	2	AD2863	dead-box ATP-depen	914	82.5	3.4	151	2	S13671	myosin catalytic 1
842	84	3.5	517	2	A84080	L-arabinose ABC tr	915	82.5	3.4	151	2	S13672	myosin catalytic 1
843	84	3.5	577	2	AD1440	hypothetical prote	916	82.5	3.4	157	1	MOHU6E	myosin alkali ligh
844	84	3.5	590	2	E83448	succinate dehydrog	917	82.5	3.4	159	2	T08067	dysenin light chain
845	84	3.5	612	2	G86405	hypothetical prote	918	82.5	3.4	236	2	T33406	hypothetical prote
846	84	3.5	643	2	H81361	ABC transport syst	919	82.5	3.4	319	2	G86869	histidinol-phospha
847	84	3.5	700	2	S38361	calpain (EC 3.4.22	920	82.5	3.4	354	2	AE0764	histidinol-phospha
848	84	3.5	709	2	C28821	1-phosphatidylinos	921	82.5	3.4	394	2	B89780	ornithine aminotra
849	84	3.5	714	2	B82959	hypothetical prote	922	82.5	3.4	399	2	G75532	acetyl-CoA acetyl
850	84	3.5	817	2	F86742	ribonuclease (limp	923	82.5	3.4	407	2	T48308	60S ribosomal prot
851	84	3.5	818	2	A42292	beta-glucosidase (924	82.5	3.4	460	2	H89907	hypothetical prote
852	84	3.5	909	2	T00009	probable primase (925	82.5	3.4	555	2	B72486	probable hydantoin
853	84	3.5	931	2	G69615	ATP-dependent DNA	926	82.5	3.4	599	2	I53395	antigen IBC-A - mo
854	84	3.5	931	2	T01372	hypothetical prote	927	82.5	3.4	617	2	C72670	hypothetical prote
855	84	3.5	1069	2	D81826	exodeoxyribonuclea	928	82.5	3.4	627	2	S31765	T-plastin - rat (f
856	84	3.5	1128	2	T42922	major single-stran	929	82.5	3.4	649	1	H64476	lipoate protein 11
857	84	3.5	1171	2	T00380	KIAA0637 protein -	930	82.5	3.4	729	1	VCLJRX	env polyprotein pr
858	84	3.5	1237	2	AE1915	hypothetical prote	931	82.5	3.4	745	1	PC4183	1-phosphatidylinos
859	84	3.5	1249	2	AE5611	myosin I myoA - Bm	932	82.5	3.4	767	2	S64571	probable membrane
860	84	3.5	1603	2	F89497	protein vit-5 (limp	933	82.5	3.4	771	2	H69305	signal-transducin
861	84	3.5	2111	2	A70668	mycocerosate synth	934	82.5	3.4	861	1	VCLJKB	env polyprotein pr
862	84	3.5	130	1	MOR11	myosin alkali ligh	935	82.5	3.4	863	1	E72259	alanine-tRNA ligas
863	83.5	3.4	341	2	T45839	probable cysteine	936	82.5	3.4	880	2	AC2108	alanyl-tRNA synth
864	83.5	3.4	349	2	A84350	hypothetical prote	937	82.5	3.4	880	2	AD1953	hypothetical prote
865	83.5	3.4	356	1	A54038	phenylalanine dehy	938	82.5	3.4	1123	2	T51517	telomerase reverse
866	83.5	3.4	357	2	F83537	4-hydroxyphenylpyr	939	82.5	3.4	1167	2	T06146	disease resistance
867	83.5	3.4	358	2	T04099	adenosylmethionine	940	82.5	3.4	1910	2	AF0394	probable adhesin h
868	83.5	3.4	462	2	D84751	hypothetical prote	941	82	3.4	109	1	PVNE5A	parvalbumin alpha
869	83.5	3.4	465	1	D70019	conserved hypochet	942	82	3.4	146	2	B71430	hypothetical prote
870	83.5	3.4	480	2	A56694	keratin, type II,	943	82	3.4	285	2	G71912	probable 3-hydroxy
871	83.5	3.4	486	2	T06907	probable ABC trans	944	82	3.4	286	2	H87292	enoyl-CoA hydrat
872	83.5	3.4	494	2	E70352	anthranilate synth	945	82	3.4	335	1	KHH0H	cathapsin H (EC 3.
873	83.5	3.4	573	2	S18181	dnak-type molecula	946	82	3.4	345	2	T11455	NADH dehydrogenas
874	83.5	3.4	678	2	G87626	DNA primase (limpor	947	82	3.4	359	1	XNEBHC	histidinol-phospha
875	83.5	3.4	678	2	C97114	recg helicase (limp	948	82	3.4	407	2	H64906	conserved hypochet
876	83.5	3.4	774	2	G71308	probable aminopept	949	82	3.4	424	2	T54454	probable molybdenu
877	83.5	3.4	870	2	F90899	hypothetical prote	950	82	3.4	434	1	S61899	hypothetical prote
878	83.5	3.4	1214	2	T47659	spliteosomal-like	951	82	3.4	458	2	A86330	hypothetical prote
879	83.5	3.4	1524	2	T30518	carbamoyl-phosphat	952	82	3.4	465	2	G86244	serine carboxypept
880	83.5	3.4	1574	2	G70466	DNA-directed RNA p	953	82	3.4	470	2	H64906	aldehyde dehydrog
881	83.5	3.4	2183	1	G48556	genome polyprotein	954	82	3.4	564	2	D83211	probable malic enz
882	83.5	3.4	2183	2	S47307	genome polyprotein	955	82	3.4	589	2	C97241	methyl-accepting c
883	83.5	3.4	2331	2	T25410	hypothetical prote	956	82	3.4	616	2	AF0263	proteinase IV (EC
884	83.5	3.4	3685	1	A27605	dystrophin, muscle	957	82	3.4	628	2	T04252	probable phosphati
885	83	3.4	153	2	T16012	hypothetical prote	958	82	3.4	651	2	F75118	probable mRNA 3'-e
886	83	3.4	216	1	BMP5BP	gldb protein - Pse	959	82	3.4	656	2	S51712	dnak-type molecula
887	83	3.4	274	2	T13010	hypothetical prote	960	82	3.4	666	2	C90464	hypothetical prote
888	83	3.4	280	2	B90536	lipoprotein (limpor	961	82	3.4	680	2	B81043	ATP-dependent DNA
889	83	3.4	298	2	A12290	cyanoaphycinase (lm	962	82	3.4	680	2	H81987	probable DNA helic
890	83	3.4	314	2	T25842	hypothetical prote	963	82	3.4	683	2	A39784	phycobillosome anch
891	83	3.4	410	2	AG2693	large terminase (l	964	82	3.4	710	2	D96728	hypothetical prote
892	83	3.4	419	2	D97475	probable large ter	965	82	3.4	786	2	H69980	single-strand DNA-
893	83	3.4	433	2	A55333	monodehydroascorba	966	82	3.4	815	2	T35970	probable efflux pr
894	83	3.4	474	2	H84210	hypothetical prote	967	82	3.4	823	2	AF3361	endopeptidase Ia (
895	83	3.4	479	1	A71303	conserved biosynth	968	82	3.4	834	2	S51006	pyruvate, water di
896	83	3.4	500	2	B83364	pyoverdine biosynt	969	82	3.4	918	2	C59226	hexokinase (EC 2.7
897	83	3.4	518	2	T22375	hypothetical prote	970	82	3.4	923	2	S44664	ZK370.3 protein -
898	83	3.4	567	2	C72698	hypothetical prote	971	82	3.4	1131	2	T47970	hypothetical prote
899	83	3.4	581	2	A75080	hypothetical prote	972	82	3.4	1166	2	T29099	reverse gyrase - S
900	83	3.4	592	2	D84431	probable endosomal	973	82	3.4	1206	2	T18557	probable hydrogena
901	83	3.4	756	1	A53943	1-phosphatidylinos	974	82	3.4	1319	1	C43735	bacc protein - Ace
902	83	3.4	764	2	T05409	hypothetical prote	975	82	3.4	1413	2	T26467	hypothetical prote
903	83	3.4	837	2	H72802	minor tail subunit	976	82	3.4	1774	2	T17421	polyketide synthas
904	83	3.4	860	1	QRHULD	IDL receptor precu	977	82	3.4	2121	2	T27406	hypothetical prote
905	83	3.4	982	2	T34830	polyketide synthas	978	82	3.4	2448	2	S53999	pyoverdine synthet

979	82	3.4	4969	2	A37113	1052	81	3.3	1051	2	T05426	hypothetical prote
980	81.5	3.4	150	1	MORUA2	1053	81	3.3	1156	2	B70356	chromosome assembl
981	81.5	3.4	150	1	MORTA2	1054	81	3.3	1173	2	T30308	rexa protein - Lac
982	81.5	3.4	152	1	MOCH6N	1055	81	3.3	1188	2	G83960	chromosome segrega
983	81.5	3.4	166	2	A28127	1056	81	3.3	1220	2	T06403	resistance complex
984	81.5	3.4	189	2	I57590	1057	81	3.3	1341	2	UG0166	LamB1 protein - L
985	81.5	3.4	194	1	MOHU01	1058	81	3.3	1421	2	T05892	hypothetical prote
986	81.5	3.4	194	1	T43507	1059	81	3.3	1421	2	T49500	hypothetical prote
987	81.5	3.4	416	2	G90305	1060	81	3.3	7962	2	T38346	elasic titin - hu
988	81.5	3.4	417	1	A34487	1061	80.5	3.3	141	2	T39245	ef-hand protein -
989	81.5	3.4	426	2	S54812	1062	80.5	3.3	202	2	T10531	S-modulin - bullfr
990	81.5	3.4	465	2	C84083	1063	80.5	3.3	236	2	C83232	probable 3-hydroxy
991	81.5	3.4	541	2	T44725	1064	80.5	3.3	309	2	T21195	hypothetical prote
992	81.5	3.4	559	2	A38604	1065	80.5	3.3	323	2	H89923	hypothetical prote
993	81.5	3.4	564	2	S44611	1066	80.5	3.3	325	2	T36851	probable transcrip
994	81.5	3.4	588	2	A25902	1067	80.5	3.3	327	2	A10039	NADPH2:quinone red
995	81.5	3.4	594	1	F64387	1068	80.5	3.3	404	2	T36791	probable acyl-CoA
996	81.5	3.4	595	2	S30389	1069	80.5	3.3	406	2	AF0097	probable membrane
997	81.5	3.4	604	2	C86282	1070	80.5	3.3	423	2	E84751	hypothetical prote
998	81.5	3.4	627	1	A35836	1071	80.5	3.3	425	2	G95877	transcription init
999	81.5	3.4	627	1	G69724	1072	80.5	3.3	426	2	S95877	probable permease
1000	81.5	3.4	739	2	B86816	1073	80.5	3.3	447	2	A83989	3-phosphoshikimate
1001	81.5	3.4	772	2	T30645	1074	80.5	3.3	466	2	F81302	hypothetical prote
1002	81.5	3.4	806	2	UC4835	1075	80.5	3.3	468	2	G89912	hypothetical prote
1003	81.5	3.4	807	2	A86740	1076	80.5	3.3	473	2	E72715	probable aspartate
1004	81.5	3.4	829	2	A99960	1077	80.5	3.3	481	2	S39682	lybl protein - Bac
1005	81.5	3.4	873	2	E90581	1078	80.5	3.3	487	2	F84751	hypothetical prote
1006	81.5	3.4	900	2	A72524	1079	80.5	3.3	495	2	D64578	conserved hypochet
1007	81.5	3.4	920	2	T43263	1080	80.5	3.3	502	2	AF1310	probable thermosta
1008	81.5	3.4	973	2	UQ0971	1081	80.5	3.3	504	2	S41661	protein disulfide-
1009	81.5	3.4	984	2	F81299	1082	80.5	3.3	522	2	F70143	hypothetical prote
1010	81.5	3.4	1208	2	T39068	1083	80.5	3.3	526	2	E89015	hypothetical prote
1011	81.5	3.4	1213	2	T19835	1084	80.5	3.3	537	2	C81362	protein B0213.15 l
1012	81.5	3.4	1312	2	S68593	1085	80.5	3.3	534	2	A83420	phosphoglycerate d
1013	81.5	3.4	1435	2	S59384	1086	80.5	3.3	537	2	B84772	membrane-bound lyl
1014	81.5	3.4	2151	1	A45389	1087	80.5	3.3	539	2	S58287	probable DnaJ prot
1015	81.5	3.4	2403	1	A59386	1088	80.5	3.3	542	1	TVH0SC	U-domain protein D
1016	81.5	3.4	2550	2	B53435	1089	80.5	3.3	546	2	T34480	protein-tyrosine k
1017	81.5	3.4	3442	2	E82589	1090	80.5	3.3	550	2	A41468	60K heat shock pro
1018	81	3.3	140	2	T28258	1091	80.5	3.3	557	2	C84146	ABC transporter re
1019	81	3.3	165	2	I40515	1092	80.5	3.3	582	2	F84807	hypothetical prote
1020	81	3.3	201	2	S05436	1093	80.5	3.3	588	2	T31675	hypothetical prote
1021	81	3.3	246	2	AB2533	1094	80.5	3.3	607	2	C69899	conserved hypochet
1022	81	3.3	248	2	T05057	1095	80.5	3.3	627	2	I49445	65K macrophage pro
1023	81	3.3	345	2	T37139	1096	80.5	3.3	672	2	T43723	dnaK-type molecula
1024	81	3.3	348	2	T12280	1097	80.5	3.3	724	2	T27858	probable peroxidas
1025	81	3.3	385	2	S39683	1098	80.5	3.3	756	1	B28821	1-phosphatidylinos
1026	81	3.3	410	1	B69611	1099	80.5	3.3	759	2	D81857	general secretion
1027	81	3.3	412	2	S69633	1100	80.5	3.3	820	2	C75284	phenylalanine-tRNA
1028	81	3.3	416	2	F97922	1101	80.5	3.3	821	2	S67087	hypothetical prote
1029	81	3.3	416	2	B95052	1102	80.5	3.3	827	1	F0MS1A	retrovirus-related
1030	81	3.3	452	2	H75379	1103	80.5	3.3	860	2	T38813	hypothetical prote
1031	81	3.3	461	2	G71818	1104	80.5	3.3	931	2	H96527	protein F27J15.16
1032	81	3.3	495	2	H71933	1105	80.5	3.3	932	2	F69552	leucyl-tRNA synthet
1033	81	3.3	538	2	G70204	1106	80.5	3.3	980	2	H84632	probable receptor-
1034	81	3.3	541	2	A84830	1107	80.5	3.3	1036	2	AG3074	cation efflux syst
1035	81	3.3	550	2	B64205	1108	80.5	3.3	1036	2	B98212	hypothetical prote
1036	81	3.3	568	2	G85654	1109	80.5	3.3	1181	2	T01799	genome polypeptid
1037	81	3.3	579	2	D90794	1110	80.5	3.3	1287	2	A43488	DNA polymerase III
1038	81	3.3	589	2	AF1788	1111	80.5	3.3	1335	2	H73511	genome polypeptid
1039	81	3.3	585	2	AB1771	1112	80.5	3.3	1762	2	T09245	CDC39 protein - ye
1040	81	3.3	585	2	AD1633	1113	80.5	3.3	2108	2	S28417	cyclic beta 1-2 gl
1041	81	3.3	627	2	H86180	1114	80.5	3.3	2870	2	H96974	calmodulin-related
1042	81	3.3	678	2	F70404	1115	80	3.3	72	2	B34669	hypothetical prote
1043	81	3.3	764	1	B8HT	1116	80	3.3	200	2	H64450	hypothetical prote
1044	81	3.3	766	1	WZBEC5	1117	80	3.3	276	2	AF1777	hypothetical prote
1045	81	3.3	783	2	C81431	1118	80	3.3	310	2	H97338	dioxygenase relate
1046	81	3.3	804	1	YFBSB	1119	80	3.3	323	2	S19650	cytochrome P450
1047	81	3.3	821	2	E95245	1120	80	3.3	348	2	T12591	NADH2 dehydrogenas
1048	81	3.3	853	2	T51505	1121	80	3.3	349	2	T31934	hypothetical prote
1049	81	3.3	993	1	PIVXCM	1122	80	3.3	360	2	H70356	conserved hypochet
1050	81	3.3	1030	2	S73944	1123	80	3.3	364	2	B83210	conserved hypochet
1051	81	3.3	1032	2	I38510	1124	80	3.3	369	2	S16482	docking protein -

1125	80	3.3	369	2	SS3703	dpa protein - Sulf	1198	79.5	3.3	826	2	T15751	hypothetical prote
1126	80	3.3	434	2	T25040	hypothetical prote	1199	79.5	3.3	952	2	S38653	transposase - Kleb
1127	80	3.3	437	2	C72600	hypothetical prote	1200	79.5	3.3	969	2	B87336	isoleucyl-tRNA syn
1128	80	3.3	455	2	S46316	aspartate transami	1201	79.5	3.3	971	2	D70128	conserved hypotet
1129	80	3.3	523	2	AC3520	galactoside transp	1202	79.5	3.3	1078	2	T18352	protein p120 - Myc
1130	80	3.3	546	2	S65596	heat shock protein	1203	79.5	3.3	1195	2	E96615	hypothetical prote
1131	80	3.3	549	2	T47069	hypothetical prote	1204	79.5	3.3	1300	2	153799	CGI protein - huma
1132	80	3.3	552	2	D90423	medium-chain-fatty	1205	79.5	3.3	1599	2	G52737	glucosyltransferas
1133	80	3.3	552	2	H70445	hypothetical prote	1206	79.5	3.3	1642	2	T08880	NMDA receptor-bind
1134	80	3.3	554	1	T03263	calcium-dependent	1207	79.5	3.3	1783	2	T42386	unconventional myo
1135	80	3.3	604	2	AF2811	methy1-accepting c	1208	79.5	3.3	2405	2	T08181	dynein alpha heavy
1136	80	3.3	615	2	G84285	succinate dehydrog	1209	79.5	3.3	3110	2	AC0116	probable virulence
1137	80	3.3	621	2	G97589	methy1-accepting c	1210	79.5	3.3	3511	2	A59295	unconventional myo
1138	80	3.3	628	2	A84649	probable glucose r	1211	79.5	3.3	3766	2	T29165	hypothetical prote
1139	80	3.3	635	2	G86744	hypothetical prote	1212	79.5	3.3	4543	1	A53102	alpha-2-macroglobu
1140	80	3.3	633	2	H71062	hypothetical prote	1213	79.5	3.3	4868	2	B54161	ryanodine-binding
1141	80	3.3	694	2	G95314	probable site-spec	1214	79.5	3.3	10223	2	TJ03225	polyketide synthas
1142	80	3.3	750	2	F90571	lipoprotein [impor	1215	79.5	3.3	1922	2	JH0171	vismnin - chicken
1143	80	3.3	782	2	T48246	ribonuclease II-li	1216	79	3.3	217	2	A42578	EF-hand calcium-bi
1144	80	3.3	806	2	T35640	probable sensor ki	1217	79	3.3	229	2	T23038	hypothetical prote
1145	80	3.3	821	2	B91110	peptidoglycan glyc	1218	79	3.3	313	2	T33849	hypothetical prote
1146	80	3.3	827	1	A36895	endopeptidase Ia (1219	79	3.3	314	2	AH1912	hypothetical prote
1147	80	3.3	831	2	B64528	conserved hypotet	1220	79	3.3	337	2	C90278	NADH2 dehydrogenas
1148	80	3.3	868	2	H81775	aconitate hydratase	1221	79	3.3	348	2	T12281	probable arginase
1149	80	3.3	875	2	T33434	hypothetical prote	1222	79	3.3	351	2	T13422	GP20 (Bacteriophag
1150	80	3.3	879	2	D85795	hypothetical prote	1223	79	3.3	355	2	AD1448	1-deoxy-d-xylulose
1151	80	3.3	879	2	H90946	hypothetical prote	1224	79	3.3	355	2	E83952	serine-CRNA ligase
1152	80	3.3	900	2	H90176	alanyl-tRNA synthet	1225	79	3.3	425	2	A71639	hypothetical prote
1153	80	3.3	924	2	G98058	hypothetical prote	1226	79	3.3	450	2	AG2431	UDP-N-acetylmurama
1154	80	3.3	963	2	T22772	hypothetical prote	1227	79	3.3	458	2	F81904	probable narX prot
1155	80	3.3	1007	2	H72734	hypothetical prote	1228	79	3.3	463	2	F70627	alpha-amylose VCAD
1156	80	3.3	1054	2	H69377	reverse gyrase (to	1229	79	3.3	466	2	B82482	probable peptidase
1157	80	3.3	1164	2	T06144	disease resistance	1230	79	3.3	467	2	B87070	pantothenate perme
1158	80	3.3	1638	2	T30313	chemotaxis protein	1231	79	3.3	474	2	D69400	hypothetical prote
1159	80	3.3	2472	2	E83594	scf11 frimeshift p	1232	79	3.3	478	2	T24805	plasmaid division p
1160	80	3.3	3530	2	A59266	unconventional myo	1233	79	3.3	483	2	T51088	conserved hypotet
1161	80	3.3	4036	2	A57099	DNA-activated prot	1234	79	3.3	493	2	E71302	60 kD chaperonin [
1162	80	3.3	4735	2	T17463	rifamycin polyketi	1235	79	3.3	542	2	B86574	cephalosporin acyl
1163	79.5	3.3	151	1	MOCH2	myosin alkali high	1236	79	3.3	558	2	S27199	bacterio-opsin act
1164	79.5	3.3	156	2	S49811	calcium-binding pr	1237	79	3.3	601	2	A84256	phosphomolylruvat
1165	79.5	3.3	157	2	A25183	myosin essential I	1238	79	3.3	603	2	C90426	flagellar hook-ass
1166	79.5	3.3	177	2	A29289	calcium-binding pr	1239	79	3.3	606	2	G64659	probable sodium/su
1167	79.5	3.3	236	2	A90190	hypothetical prote	1240	79	3.3	610	2	H83165	hypothetical prote
1168	79.5	3.3	242	2	B70155	spoIIIV-associate	1241	79	3.3	613	2	H85363	phosphotransferase
1169	79.5	3.3	256	2	G69997	hypothetical prote	1242	79	3.3	632	2	AG1366	hypothetical prote
1170	79.5	3.3	271	1	A60253	calixectin - human	1243	79	3.3	632	2	S64786	cation-transporin
1171	79.5	3.3	277	2	F82388	transcription regu	1244	79	3.3	673	2	AG3521	probable single-str
1172	79.5	3.3	307	2	AE3135	hypothetical prote	1245	79	3.3	684	2	E75434	hypothetical prote
1173	79.5	3.3	307	2	G98152	hypothetical prote	1246	79	3.3	686	2	T27826	protein ZC373.1 [I
1174	79.5	3.3	421	2	A83139	flagellar hook ass	1247	79	3.3	696	2	H89621	calpain (EC 3.4.22
1175	79.5	3.3	426	2	A70444	preprotein translo	1248	79	3.3	700	1	CIH0H2	retrovirus-related
1176	79.5	3.3	430	2	S30115	aspartate-cRNA lig	1249	79	3.3	717	2	S31034	GGDEF family prote
1177	79.5	3.3	438	2	B64494	probable permease	1250	79	3.3	724	2	AH3153	hypothetical prote
1178	79.5	3.3	438	2	AF0963	conserved hypotet	1251	79	3.3	737	2	D98154	DNA mismatch repai
1179	79.5	3.3	464	2	B72260	deoxyribopyrimidin	1252	79	3.3	788	2	E97188	ubiquitin carboxyl
1180	79.5	3.3	479	2	AF2146	probable iron-sulf	1253	79	3.3	801	2	A47744	protein R09H3.1 [I
1181	79.5	3.3	481	1	B64537	dhak-c-type molecu	1254	79	3.3	811	2	S76690	class IV chitin sy
1182	79.5	3.3	571	2	C70353	succinate dehydrog	1255	79	3.3	813	2	G75531	hypothetical prote
1183	79.5	3.3	596	2	T29361	hypothetical prote	1256	79	3.3	860	2	G70623	probable sensor pr
1184	79.5	3.3	599	2	AB1906	hypothetical prote	1257	79	3.3	865	2	AB3547	probable aconitate
1185	79.5	3.3	619	2	E81117	dihydroxy-acid deh	1258	79	3.3	919	2	T16693	Arm repeat contain
1186	79.5	3.3	637	2	H85043	hypothetical prote	1259	79	3.3	928	2	T47846	ubiquitin carboxyl
1187	79.5	3.3	651	2	S46302	dhak-c-type molecu	1260	79	3.3	979	2	T41006	protein R09H3.1 [I
1188	79.5	3.3	651	2	T48271	ribonucleotide red	1261	79	3.3	1073	2	F89467	hypothetical prote
1189	79.5	3.3	693	2	A70431	H+/K+-exchanging A	1262	79	3.3	1204	2	T18812	class IV chitin sy
1190	79.5	3.3	696	2	A70431	DNA topoisomerase	1263	79	3.3	1239	2	T42020	hypothetical prote
1191	79.5	3.3	701	2	T46846	5-methyltetrahydro	1264	79	3.3	1633	2	T14758	related to Nup98-N
1192	79.5	3.3	710	2	F86778	phosphoribosylform	1265	79	3.3	1844	2	T51890	centromere protein
1193	79.5	3.3	734	2	E72271	hypothetical prote	1266	79	3.3	2663	1	S28261	protein g377 - mal
1194	79.5	3.3	737	2	S55117	geloslin, secreted	1267	79	3.3	3119	2	T18414	probable membrane
1195	79.5	3.3	739	2	T51701		1268	79	3.3	4910	2	S64942	
1196	79.5	3.3	785	2	S46672		1269	79	3.3	141	2	S01772	
1197	79.5	3.3	790	2	A53909		1270	78.5	3.2	141	2		

1271	78.5	3.2	150	1	MORB2	1344	78	3.2	433	2	H8760	peptidoglycan-bind
1272	78.5	3.2	160	2	A25571	1345	78	3.2	438	2	G71094	aspartate-tRNA lig
1273	78.5	3.2	185	1	MOC4E	1346	78	3.2	459	2	E97786	dihydroliopamide d
1274	78.5	3.2	192	1	MORB1	1347	78	3.2	459	2	D86810	hypothetical prote
1275	78.5	3.2	299	2	D8306A	1348	78	3.2	474	2	D84372	dihydroliopamide d
1276	78.5	3.2	301	2	B83512	1349	78	3.2	475	2	A71110	hypothetical prote
1277	78.5	3.2	335	2	S32908	1350	78	3.2	466	2	S78514	conserved hypochet
1278	78.5	3.2	338	2	A99416	1351	78	3.2	502	2	T35743	ribosomal protein
1279	78.5	3.2	339	2	C83264	1352	78	3.2	523	2	E72314	ribosome ABC transpo
1280	78.5	3.2	335	2	B72053	1353	78	3.2	529	2	S57345	m-impartin (nuclea
1281	78.5	3.2	335	2	B86568	1354	78	3.2	535	1	SY88TP	CTP synthase (BC 6
1282	78.5	3.2	335	2	AF1125	1355	78	3.2	544	2	S61300	heat shock protein
1283	78.5	3.2	335	2	AE1486	1356	78	3.2	572	2	P90564	conserved hypochet
1284	78.5	3.2	333	1	G69869	1357	78	3.2	592	2	S61503	beta-fructofuranos
1285	78.5	3.2	331	2	T34692	1358	78	3.2	592	2	QJ0091	beta-fructofuranos
1286	78.5	3.2	389	2	T29410	1359	78	3.2	606	2	G71853	flagellar hook-ass
1287	78.5	3.2	402	2	G96784	1360	78	3.2	619	2	A10385	1-deoxy-D-xyliose
1288	78.5	3.2	411	2	S41945	1361	78	3.2	626	2	H82266	1-deoxyxylulose-5-
1289	78.5	3.2	434	2	E97026	1362	78	3.2	627	2	A97420	probable acyl-CoA
1290	78.5	3.2	437	2	T48390	1363	78	3.2	627	2	AB2638	acyl-CoA dehydroge
1291	78.5	3.2	441	2	E72579	1364	78	3.2	643	2	S49303	dnak-type molecula
1292	78.5	3.2	441	2	T43544	1365	78	3.2	647	2	T41121	heat shock protein
1293	78.5	3.2	461	2	H83130	1366	78	3.2	649	2	TJ01515	dnak-type molecula
1294	78.5	3.2	507	2	B87400	1367	78	3.2	664	2	TS2121	acyl-CoA oxidase (
1295	78.5	3.2	512	2	G72476	1368	78	3.2	669	1	S74436	DNA ligase (NAD) (
1296	78.5	3.2	514	2	T25534	1369	78	3.2	690	2	B42594	D-amino acid hydraz
1297	78.5	3.2	550	2	T39942	1370	78	3.2	691	2	B81937	competence protein
1298	78.5	3.2	553	2	C70946	1371	78	3.2	717	2	S31035	retrovirus-related
1299	78.5	3.2	554	2	T15992	1372	78	3.2	810	2	S75931	hypothetical prote
1300	78.5	3.2	560	2	D72478	1373	78	3.2	822	2	AB2507	hypothetical prote
1301	78.5	3.2	574	2	AF0167	1374	78	3.2	894	1	FAHUA2	alpha-actinin 2 -
1302	78.5	3.2	580	2	AF1292	1375	78	3.2	900	2	F71426	hypothetical prote
1303	78.5	3.2	586	2	T36252	1376	78	3.2	914	1	UN0550	iodide peroxidase
1304	78.5	3.2	600	2	C95113	1377	78	3.2	1036	2	JC5568	serine proteinase
1305	78.5	3.2	607	2	AH0044	1378	78	3.2	1040	1	A38306	alpha-mannosidase
1306	78.5	3.2	643	2	D70697	1379	78	3.2	1081	2	T31094	surface antigen B8
1307	78.5	3.2	660	2	E83656	1380	78	3.2	1092	2	T45095	probable arabinosy
1308	78.5	3.2	663	2	AE3290	1381	78	3.2	1132	2	A35089	myosin-binding pro
1309	78.5	3.2	672	2	T34899	1382	78	3.2	1188	2	F64367	pyruvate, water di
1310	78.5	3.2	666	2	S61502	1383	78	3.2	1203	2	D86625	subunit A of ATP-d
1311	78.5	3.2	710	2	AC0999	1384	78	3.2	1285	2	T12796	probable transglyc
1312	78.5	3.2	717	2	AC1419	1385	77.5	3.2	1260	2	G87408	glucanase 5-dehydr
1313	78.5	3.2	728	2	S59642	1386	77.5	3.2	281	2	S34545	hypothetical prote
1314	78.5	3.2	746	2	AF0845	1387	77.5	3.2	313	2	H69297	conserved hypochet
1315	78.5	3.2	752	2	G69457	1388	77.5	3.2	331	2	D86413	cysteine proteinas
1316	78.5	3.2	807	2	E90523	1389	77.5	3.2	345	2	D88485	protein F23F12.4 (
1317	78.5	3.2	820	2	D81382	1390	77.5	3.2	373	2	B95291	conserved hypochet
1318	78.5	3.2	868	2	C81200	1391	77.5	3.2	385	2	T32356	hypothetical prote
1319	78.5	3.2	884	2	D85817	1392	77.5	3.2	388	2	S24926	coat protein, 41K
1320	78.5	3.2	885	1	S78246	1393	77.5	3.2	390	1	G64500	probable hexosyltr
1321	78.5	3.2	901	1	FAHUA3	1394	77.5	3.2	407	2	C96978	tyrosyl-tRNA synth
1322	78.5	3.2	906	2	S25852	1395	77.5	3.2	416	2	C96683	F12P19.7 (imported
1323	78.5	3.2	921	2	TS1804	1396	77.5	3.2	422	1	A32306	cytochrome P450 CY
1324	78.5	3.2	933	2	A75541	1397	77.5	3.2	432	1	D64773	trigger factor (va
1325	78.5	3.2	1196	2	H87542	1398	77.5	3.2	432	2	B85540	hypothetical prote
1326	78.5	3.2	1604	2	B86287	1399	77.5	3.2	432	2	B90690	trigger factor (lm
1327	78.5	3.2	1847	2	E64477	1400	77.5	3.2	443	2	AB1405	probable phosphoes
1328	78.5	3.2	2132	2	B75009	1401	77.5	3.2	450	1	S13730	pmba protein - Esc
1329	78.5	3.2	2554	1	TVFPTL	1402	77.5	3.2	450	2	D86121	maturation of anti
1330	78.5	3.2	5005	2	F82884	1403	77.5	3.2	466	2	D91280	maturatin of anti
1331	78.5	3.2	7576	2	T17428	1404	77.5	3.2	466	2	S16333	nicotinic acetylch
1332	78	3.2	210	2	T41082	1405	77.5	3.2	470	2	G97103	aspartate ammonia-
1333	78	3.2	301	2	H71011	1406	77.5	3.2	470	2	D86848	hypothetical prote
1334	78	3.2	318	2	G82416	1407	77.5	3.2	487	2	S73161	hypothetical prote
1335	78	3.2	322	2	A57516	1408	77.5	3.2	494	2	S67166	PAC1 protein - yea
1336	78	3.2	337	2	S50442	1409	77.5	3.2	532	2	A96904	ABC1 family protei
1337	78	3.2	362	1	KHRZOG	1410	77.5	3.2	538	2	E85438	step II splicing f
1338	78	3.2	367	1	KHRZOG	1411	77.5	3.2	554	2	AB0295	dolichyl-phosphate
1339	78	3.2	384	2	S14450	1412	77.5	3.2	555	2	S60201	multicopy suppress
1340	78	3.2	404	2	B72409	1413	77.5	3.2	556	2	A11394	arginyl tRNA synth
1341	78	3.2	408	2	D67417	1414	77.5	3.2	581	2	I49669	FKBP5 binding pro
1342	78	3.2	417	2	AG3571	1415	77.5	3.2	594	2	A86309	F20D23.3 protein -
1343	78	3.2	428	2	G97607	1416	77.5	3.2	595	1	B69893	propionyl-CoA carb

1417	77.5	3.2	600	2	B97982	group B oligopepti
1418	77.5	3.2	617	2	AF2897	conserved hypotet
1419	77.5	3.2	619	2	C81905	probable dihydroxy
1420	77.5	3.2	633	2	D64222	DNA topoisomerase
1421	77.5	3.2	634	2	S56817	probable succinate
1422	77.5	3.2	637	1	YSCR1	acetoacetate synth
1423	77.5	3.2	641	2	H97672	hypothetical prote
1424	77.5	3.2	642	2	D71909	ferrous iron trans
1425	77.5	3.2	645	2	A25089	diak-type molecula
1426	77.5	3.2	648	2	S53458	diak-type molecula
1427	77.5	3.2	651	2	D70789	probable acetyl-co
1428	77.5	3.2	651	2	F71013	hypothetical prote
1429	77.5	3.2	672	2	AF3318	RNA polymerase sig
1430	77.5	3.2	681	2	E64908	peptidyl-dipeptida
1431	77.5	3.2	681	2	C90897	dipeptidyl carboxy
1432	77.5	3.2	681	2	D85720	dipeptidyl carboxy
1433	77.5	3.2	696	2	D95206	hypothetical prote
1434	77.5	3.2	773	2	D75031	hydrogenase expres
1435	77.5	3.2	793	2	T27133	hypothetical prote
1436	77.5	3.2	827	2	E64607	DNA gyrase, sub A
1437	77.5	3.2	828	2	D81522	DNA mismatch repai
1438	77.5	3.2	828	2	C86608	DNA mismatch repai
1439	77.5	3.2	828	2	G72017	DNA mismatch repai
1440	77.5	3.2	848	2	E71404	hypothetical prote
1441	77.5	3.2	879	2	AC1680	pyruvate phosphate
1442	77.5	3.2	885	2	AD1865	hypothetical prote
1443	77.5	3.2	895	1	PAFPA	alpha-actinin - fr
1444	77.5	3.2	909	2	C97325	hypothetical prote
1445	77.5	3.2	916	2	F97053	penicillin-binding
1446	77.5	3.2	944	2	T03826	cytochrome b245 be
1447	77.5	3.2	956	2	AB1761	exonuclease ABC (
1448	77.5	3.2	963	2	C90535	conserved hypotet
1449	77.5	3.2	977	2	D96665	protein F22C12.18
1450	77.5	3.2	1025	2	G85834	hypothetical prote
1451	77.5	3.2	1025	2	D90989	hypothetical prote
1452	77.5	3.2	1035	1	GNLJG6	HIV-1 retroprotein
1453	77.5	3.2	1172	2	D72482	probable antibioli
1454	77.5	3.2	1207	2	H87475	urea amidolyase-re
1455	77.5	3.2	1233	2	T30534	chromosome segrega
1456	77.5	3.2	1324	2	T01508	mismatch repair en
1457	77.5	3.2	1435	2	S54697	DNA polymerase III
1458	77.5	3.2	1486	2	E85618	hypothetical prote
1459	77.5	3.2	1541	2	AG2474	heterocyst glycoli
1460	77.5	3.2	1652	2	T16789	hypothetical prote
1461	77.5	3.2	2037	2	S37178	fatyl-acyl-CoA syn
1462	77.5	3.2	2543	2	F69679	polyketide synthas
1463	77.5	3.2	3429	2	T13853	hypothetical prote
1464	77.5	3.2	5138	2	B96695	hypothetical prote
1465	77.5	3.2	142	2	D90269	conserved hypotet
1466	77.5	3.2	150	2	B23253	myosin A2 catalyti
1467	77.5	3.2	188	2	A23253	myosin A1 catalyti
1468	77.5	3.2	198	2	S28860	clytin - hydromedu
1469	77.5	3.2	232	2	E82482	antibiotic acetyl
1470	77.5	3.2	247	2	AB0121	quorum-sensing tra
1471	77.5	3.2	277	2	JM0102	azaarene carbazole
1472	77.5	3.2	281	2	H64125	modd protein homol
1473	77.5	3.2	300	1	D34443	nitrogen fixation
1474	77.5	3.2	300	2	AD1988	nitrogen fixation
1475	77.5	3.2	318	2	G95255	rim-barrel protein
1476	77.5	3.2	321	2	S54403	1-phosphatidylinos
1477	77.5	3.2	344	2	T12247	NADH dehydrogenas
1478	77.5	3.2	347	2	E64069	ycog protein homol
1479	77.5	3.2	347	2	A12010	two-component hybr
1480	77.5	3.2	357	2	A75044	translational initia
1481	77.5	3.2	357	2	AF1729	protein gp20 (Bact
1482	77.5	3.2	359	2	F83828	hypothetical prote
1483	77.5	3.2	370	2	AH2629	2'-deoxycytidine 5
1484	77.5	3.2	370	2	E97411	hypothetical prote
1485	77.5	3.2	380	2	D64903	probable arylsulfa
1486	77.5	3.2	390	2	C85726	probable enzyme Z2
1487	77.5	3.2	390	2	F90891	probable enzyme [1
1488	77.5	3.2	399	1	D64327	H+-transporing tw
1489	77.5	3.2	409	2	T46741	arginine deiminase

1490	77	3.2	409	2	T35155	hypothetical prote
1491	77	3.2	425	2	S32866	outL protein - Brw
1492	77	3.2	432	2	E96880	hypothetical prote
1493	77	3.2	433	2	S77508	extra protein - Syn
1494	77	3.2	438	2	A75071	aspartyl-tRNA synt
1495	77	3.2	455	2	D75043	seryl-tRNA synthet
1496	77	3.2	458	1	QOEGC4	pabC intron protei
1497	77	3.2	492	1	T03271	calcium-dependent
1498	77	3.2	493	1	JC4372	IMP dehydrogenase
1499	77	3.2	505	2	G86391	hypothetical prote
1500	77	3.2	506	1	S22975	cytochrome P450 52

ALIGNMENTS

RESULT 1
T50686
peroxisomal Ca-dependent solute carrier (imported) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50686
R:Weber, F.E.; Minestrini, G.; Dyer, J.H.; Weider, M.; Boffelli, D.; Compassi, S.; Wehr, Proc. Natl. Acad. Sci. U.S.A. 94, 8509-8514, 1997
A:Title: Molecular cloning of a peroxisomal Ca2+-dependent member of the mitochondrial c
A:Reference number: Z25180; MUID:97385133; PMID:9238007
A:Accession: T50686
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-475 <WEB>
A:Cross-references: UNIPROT:O18757; EMBL:AF004161; PDB:1AAB69156.1
C:Keywords: peroxisome

Query Match 61.7%; Score 1494; DB 2; Length 475;
Best Local Similarity 66.7%; Pred. No. 1, se-94;
Matches 279; Conservative 64; Mismatches 73; Indels 2; Gaps 1;
Qy 52 KQKIVAGDQDLDGDFEFVHYLDHEKKLVRLKLDKNDGRDAQEIQSLDGL 111
Db 60 EKKIFPTGVNKGKLDFFEFMYKLDHEKKMLAFKSLDKNDGKLEASIVQSLQTLG 119
Qy 112 VKTSEQAEKILKSMKNGKMTIDMNMWRDYLHPENIPETILYWKSTIPDVGENTL 171
Db 120 LTTSEQAEILITSDIDAGMTVDNMBWRDYLFPNVADEILIRKWKSTIGIDGSLT 179
Qy 172 VPDEFTEERQOTGMWRHLVAGGAGAVSRTCTAPLDRLKVLQVNASRNNMGIVGFT 231
Db 180 IPDEFTEERKSGQWRQLLAGIAGVSRSTAPLDRLKVMQVHGSKS -WNITGGFR 237
Qy 232 QMRREGASLRNGINGINVLKIPESAIKPMAYEQIKRLVGSQDETLRIHERLVAGSLAG 291
Db 238 QMRREGASLRNGINGINVLKIPESAIKPMAYEQIKRLVGSQDETLRIHERLVAGSLAG 297
Qy 292 AINQSSLYPMEVLTAKTMALRKTOYGSMDCARILABEGVAFYGYVPMGLIIPYAG 351
Db 298 AINQSSLYPMEVLTAKTMALRKTOYGSMDCARILABEGVAFYGYVPMGLIIPYAG 357
Qy 352 IDLAIVETLKNAMLOHYAVNSADPGFVLVLAAGTMSSTGQSLASPLATVRTMQAASI 411
Db 358 IDLAIVETLKNAMLOHYAVNSADPGFVLVLAAGTMSSTGQSLASPLATVRTMQAASI 417
Qy 412 EGAPVYTMSSLPFHILRTSGAFGLYGLAPNFKVLPANVSYVYVENLKITLGVQSR 469
Db 418 EGAPVYTMSSLPFHILRTSGAFGLYGLAPNFKVLPANVSYVYVENLKITLGVQSR 475

RESULT 2
T22688
hypothetical protein F55A11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22688
R:Kerhaw, J.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19600

A:Accession: T22688

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-588 <MIL>

A:Cross-references: UNIPROT:Q20799; EMBL:Z72511; PIDN:CAA96658.1; GSPDB:GN00023; CESP:F5

A:Experimental source: clone F55A11

C:Genetics:

A:Gene: CESP:F55A11.4

A:Map position: 5

A:Insertions: 24/1; 77/2; 277/3; 434/3; 474/1; 511/3; 531/3

Query Match 48.6%; Score 1177.5; DB 2; Length 588;

Best Local Similarity 49.0%; Pred. No. 8.4e-73;

Matches 220; Conservative 97; Mismatches 107; Indels 25; Gaps 4;

QY 22 ESKGLPAELKSTIKLSVFIIPSQEFSTYRQWKQIVQAGDLDGQDLDFEFVHYLDHDK 81

DB 105 ETPHIAPIAPV-----IMSKSPDDEGRVDFVSFSSVLENEQ 143

QY 82 KRLVFKRIDKDKGRIDAGEIMQSLRDIGVKISEQOAEKILKSPDKNGTMTIDNEMRD 141

DB 144 KLAEMFADMDRNDGLVDVEMKNYCKDIGVPLDDHKAQHTVKNMDQTSASVDLKEFQZ 203

QY 142 YHLHVEVNIPEIILYKSHSTIPDVGENLTVPDEFVEERQTMWRHLVAGGAGAVSR 201

DB 204 FMWLFPSSDLKIDVDFWRHNLIDIGEDSQIPEDFSQEMQEGIMWRHLVAGGAAGAVSR 263

QY 202 TCTAPDLKLVLMQVHASRNNMGIVGFTQMTREGARSLRNGNGINVLKIPESAIKF 261

DB 264 TCTAPDRLIKVYLQVNSSKTNRLGWSCLKLHAEGGKSPFRNGNGINVLKIPESAIKF 323

QY 262 MAYEJOIKRLVGSDO--ETLIRHERLVAGSLAGIAOSSIYPMVEVLKTRMALRKTGOVS-G 318

DB 324 MCDQLKRLQKKKGHEISTFRLCNSHAGAISSGTTIPMEVMTKRLAKRTGQLDRG 383

QY 319 MDCARRILAREGVAAFYKGYVNMGLIIPYAGIDLAIVETTLKNAVLQHYAVNSADPGVF 378

DB 384 IIFPAIKMYIKKEGIRGKYKYLNLGIIPYAGIDLAIVETTLKRYVRYETNSSEGV 443

QY 379 VLLACGTMSSTCGQLASYPALVTRTMOAQSIEGAPV-TMSLFFHILRTGAGLYR 437

DB 444 ALACGTCSSTCGQLSSYPALVTRTMOAQSIEGAPV-TMSLFFHILRTGAGLYR 503

QY 438 GLAPNFMKVPAYSISYVVENKLTITGV 466

DB 504 GITPNEFLKVPAYSISYVVEKVRITGLGV 532

RESULT 3

protein F17E5.2 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001

C:Accession: G89667

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/genC/elegans/ and www.sanger.ac.uk/Projects/C_ele

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: G89667

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-531 <STO>

A:Cross-references: GB:chr_X; PIDN:CAA90761.1; PID:g3876012; GSPDB:GN00028; CESP:F17E5.2

C:Genetics:

A:Gene: F17E5.2

A:Map position: X

Query Match 42.5%; Score 1030.5; DB 2; Length 531;

Best Local Similarity 45.3%; Pred. No. 8.2e-63;

Matches 208; Conservative 95; Mismatches 103; Indels 53; Gaps 9;

QY 29 ELKSTIKLSVFIIPSQEFSTYRQWKQIVQAGDLDGQDLDFEFVHYLDHDKRLVFK 88

DB 36 DLQALSLQAHPIASV-----APKILBRMSSEHSDRTYADFTNYVLAHEKRLAEVFD 90

QY 89 ILDKKNDGRIDAGEIMQSLRDIGVKISEQOAEKILKSPDKNGTMTIDNEMRDYHLHPV 148

DB 91 KIDLNSDGEVDMAEIKSYCKEMGVNLDQKAMSVKMQQSGSSVNLNEFQDFMILYPS 150

QY 149 ENIPEIILYKSHS-----TIFDVGENLTVPDEFVEERQTMWRHLV 191

DB 151 TDMRDVDFWRHNLVCTCLESNSRFTQNFQIIDIGEDQVPEDFTPQELSGVMRHLV 210

QY 192 AGGAGAVSRCTAPDLRLKV-----LMQVHASRNNMGIVGFTQMT 234

DB 211 AGGVAGAMSRCTCAPDRLIKVYLQVWYVHLHFRIMFLKALQVNSTRTNKLGVSCVHLH 270

QY 235 REGARSLRNGNGINVLKIPESAIKFMAVEQIKRLV-----GSDQETLIRHERLVAGSL 289

DB 271 AEGGKSPFRNGNGINVLKIPESAMKFCYDQIKRMQOEYKGAELSTI---ERLLAGSS 327

QY 290 AGIAOSSIYPMVEVLKTRMALRKTGOY--SGMLDCARRILAREGVAAFYKGYVNMGLITP 348

DB 328 AGAISQALYPMVEVMTKRLAKRTGQLDKGMFHFAMKMTTKSGIKCTGYLPLNLGITP 387

QY 349 YAGIDLAIVETTLKNAVLQHYAVNSADPGFVLACGTMSSTCGQLASYPALVTRTMOA 408

DB 388 YAGIDLVYESLKSMTKTYTHT--EPGVLLACGTCSSTCGQLASYPALVTRTLOAR 446

QY 409 A-SIEGAPV-TMSLFFHILRTGAGLYRGLAPNFMK 445

DB 447 AISPKNSTQPDITWVGQFKHILQTEGFTGLRGITPFMK 485

RESULT 4

T21074

hypothetical protein F17E5.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T21074

R:McMurray, A.

submitted to the EMBL Data Library, August 1995

A:Reference number: Z19368

A:Accession: T21074

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-587 <MIL>

A:Cross-references: EMBL:Z50873; PIDN:CAA90761.2; GSPDB:GN00028; CESP:F17E5.2

A:Experimental source: clone F17E5

C:Genetics:

A:Gene: CESP:F17E5.2

A:Map position: X

A:Insertions: 21/1; 48/3; 74/2; 111/3; 183/2; 384/1; 432/3; 503/1; 541/3

Query Match 42.5%; Score 1030.5; DB 2; Length 587;

Best Local Similarity 45.3%; Pred. No. 9.3e-63;

Matches 208; Conservative 95; Mismatches 103; Indels 53; Gaps 9;

QY 29 ELKSTIKLSVFIIPSQEFSTYRQWKQIVQAGDLDGQDLDFEFVHYLDHDKRLVFK 88

DB 94 DLQALSLQAHPIASV-----APKILBRMSSEHSDRTYADFTNYVLAHEKRLAEVFD 146

QY 89 ILDKKNDGRIDAGEIMQSLRDIGVKISEQOAEKILKSPDKNGTMTIDNEMRDYHLHPV 148

DB 147 KIDLNSDGEVDMAEIKSYCKEMGVNLDQKAMSVKMQQSGSSVNLNEFQDFMILYPS 206

QY 149 ENIPEIILYKSHS-----TIFDVGENLTVPDEFVEERQTMWRHLV 191

DB 207 TDMRDVDFWRHNLVCTCLESNSRFTQNFQIIDIGEDQVPEDFTPQELSGVMRHLV 266

QY 192 AGGAGAVSRCTAPDLRLKV-----LMQVHASRNNMGIVGFTQMT 234

Db 267 AGVAGAMSRCTAPDRIRKYLQVMTLHFLHIMFLKALQVNSTKTNKLGVSCVHLH 326
 QY 235 REGGABSLMNGNGINVLKIPESAIKEMAYEQIRLV-----GSDQETLRHHELVAGSL 289
 Db 327 AEGGKISFMWNGINVLKIPESAMKFCYDQIRKMOEYKGAELSTI---ERLLAGSS 383
 QY 290 AGAIAOSSIPMEVLTAKRMALRKTQY-SCMLDCARRILAREGVAAPFYKGVPMMLGIIP 348
 Db 384 AGAISQAIITPMEMKTRMLARRTGQDLKGMFHNHMYKTEGKICFYKGLPPLGLIIP 443
 QY 349 YAGIDLAIVETLKNXLAQHYAVNSADPGVFLVLAAGTMSSTCGQLASYPALVTRTMOAQ 408
 Db 444 YAGIDLVETLSKMYKYTEHT-EPGVALLAACGTCSSTCGQLASYPALVTRTMOAR 502
 QY 409 A-SIEGAPAV-TMSLTKHILRTGAGLYRGLAPNPMK 445
 Db 503 AISPKNSTOPTWVGQPKHILQTEGTGLYRGITPNPMK 541

RESULT 5

T49871
 peroxisomal Ca-dependent solute carrier-like protein - Arabidopsis thaliana
 N/Alternate names: protein T211.30
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C/Accession: T49871
 R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le
 submitted to the Protein Sequence Database, April 2000
 A/Reference number: Z24493
 A/Accession: T49871
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-479 <BEV>
 A/Cross-references: UNIPROT:Q9LY28; EMBL:AL163912; GSPDB:GN00063; ATSP:T211.30
 A/Experimental source: cultivar Columbia; BAC clone T211
 C/Genetics:
 A/Map position: 5
 A/Intons: 133/1; 391/1; 421/2
 C/Keywords: peroxisome

Query Match 34.0%; Score 825; DB 2; Length 479;
 Best local similarity 38.9%; Pred. No. 7.9e-49;
 Matches 175; Conservative 103; Mismatches 148; Indels 24; Gaps 9;
 QY 18 FOYFESKGLP-AELKSIFFK--LSVFIPOEFSTYRQMKIVQAGDKDLDGQDLFEEFVH 74
 Db 42 FDFPDNSNLGFLDYAQLEKGLASLQIPPE-----YKVARDLFRVCANRDGRVDVQEFRR 96
 QY 75 YLDQHEKKLVFKILDKNDGRIDAOEIMOSLBDLVKISSEQAEEKILKSMQKGTMTI 134
 Db 97 YIAKELVELRIFOAIIVENHGCILPELWELVAKAIEIDDELAIFVEHVDKDNNGTI 156
 QY 135 DNNEBMRDYLHLHPVE-NIPETILYWKSTIFDVGENLTVPDEFVBERQSGMMRHLVAG 193
 Db 157 TFEEMRDFLLYPRHEATLENITHHMERVCLDIDEGQVIFPGISKHYKRS---RLLLAG 212
 QY 194 GGAGAVSRCTAPDLRLKVLMOVHASSNNMGIVGFTOMIREGASRLWNGINVLKI 253
 Db 213 GLGAVSRTATAPDLRLKVLMOVRAHA---GVLPTIKIIRBDKLMGFRNGNLNWKV 269
 QY 254 APBSAIFMAVEQIKRLVSGDQETLRHRLVAGSLAGALAQSSIIYMEVLTAKRM--ALR 311
 Db 270 APBSAIFCAVEMLKPMIGGEDGIGTSRLMAGMAGALAQTIYPMDLVKTRLQTCVS 329
 QY 312 KTGQSGMLDCARRILAREGVAAPFYKGVPMMLGIIPYAGIDLAIVETLKNXLAQHYAVN 371
 Db 330 EGGKAPKMLKTKIWIWREGRAPYKGLFPSLLAIVPAGIDLAIVETLKNL-SRTYILQ 388
 QY 372 SADPGVFLVLAAGTMSSTCGQLASYPALVTRTMOAQASIEGABVTMSLFKHILRTG 431
 Db 389 DTEBGPILQISCGMTSGALGASCVYPLQVAVTRTMOADS-----KTMQKEGFMMTMKGG 443

QY 432 AFGYRGLAPNPMKVIPAVSIYVVENLK 461
 Db 444 LRGFYRGLPNLKVPAPASITIVYEMAK 473

RESULT 6

T01729
 mitochondrial solute carrier protein homolog - Arabidopsis thaliana
 N/Alternate names: protein A_IG002N01.16
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
 C/Accession: T01729
 R/Scheet, P.; Maggii, L.
 submitted to the EMBL Data Library, June 1997
 A/Description: The sequence of A. thaliana IG002N01.
 A/Reference number: Z14407
 A/Accession: T01729
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-352 <SCH>
 A/Cross-references: UNIPROT:O04619; EMBL:AF007269; NID:g2191126; PID:g2191150
 A/Experimental source: cultivar Columbia
 C/Genetics:
 A/Map position: 4
 A/Intons: 51/2; 67/3; 122/2; 135/1; 172/3; 210/3; 325/3
 A/Note: A_IG002N01.16
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: mitochondrion

Query Match 21.4%; Score 519; DB 2; Length 352;
 Best local similarity 37.3%; Pred. No. 4.4e-28;
 Matches 116; Conservative 61; Mismatches 104; Indels 30; Gaps 7;

QY 188 RHLVAGGAGAVSRCTAPDLRLKVLMOVHASS-NMGIVGFTOMIREGASRLWNG 246
 Db 40 KSLFAGGAVGAVSRITAVAPLEPMKILLQVNPPIKXSGTVQGLKHWREGGLRFGKN 99
 QY 247 GINVLKIPESAIKEMAYEQ-----IKRLVSGDQETLRHRLVAGSLAGALAQSSI 298
 Db 100 GTQCARIVPNSAVKFSYEQASNGILYMYRQRTGENAQLTPLRLAGAGATGILANSAT 159
 QY 299 YPMSEVLTAKRMALRKTG---QYSGMLDCARRILAREGVAAPFYKGVPMMLGIIPYAGIDLA 355
 Db 160 YPMDMWRGLITVQTANSFYRIGIAHALATVLAEBGRALYRGLVGVIVGVGLNFS 219
 QY 356 VYETLKNXLAU-----QHVAVNSADPGVFLVLAAGTMSSTCGQLASYPALVTRTMO----- 406
 Db 220 VYESTLKD-WLVKENPYGLVENNELTVTRLTGALAGTVQOTIAYPLDVIRRMQWGMK 278
 QY 407 -AQASIEGAEVY-----MSLFKHILRTGAGLYRGLAPNPMKVIPAVSIYVYE 458
 Db 279 DASAIYVGEERSFASLEYTGMDAFKRTVHBEGFALYKGLVPSVSKVPSIALAFVTE 338
 QY 459 NLKITLGVQSR 469
 Db 339 MKVDVLGVEFR 349

RESULT 7

T39385
 probable mitochondrial carrier protein - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
 C/Accession: T39385
 R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
 submitted to the EMBL Data Library, January 1999
 A/Reference number: Z21850
 A/Accession: T39385
 A/Molecule type: DNA
 A/Residues: 1-500 <LYN>
 A/Cross-references: UNIPROT:O94502; EMBL:AL035085; PIDN:CAA22679.1; GSPDB:GN00067; SPDB:
 A/Experimental source: strain 972h-; cosmid c12D12
 C/Genetics:

A;Gene: SPDB:SPBC12D12.05C
A;Map position: 2
A;introns: 54/3; 426/2
C;Keywords: mitochondrion

Query Match 19.7%; Score 477; DB 2; Length 500;
Best Local Similarity 35.7%; Pred. No. 5.2e-25;
Matches 128; Conservative 57; Mismatches 120; Indels 54; Gaps 13;

QY 146 HVENIPERIT-LYWKST-----IPDVGNLTVPDEFTVERQGMWRLVAGCGAGAV 199
DB 83 HPHHNDSTIPASMHDTPMKLVFRLQNL--PDGGLLENDPKXNVGFIISGAGIIV 140
QY 200 SRTCTAPLRLKYL-----QVHASNNGIVGFTQMIREGASLW 243
DB 141 SRTCTAPLRLKYLISDTGSKPSPKYPATLLHTTK-----VLMNRGIRSF 189
QY 244 RKGGINVLKAPSAIKFMAVEQIKRLVG--SDQETLRHERL---VAGSLAGAIQSS 238
DB 190 VGGINVLKYMPSISIKFGTYEAMKRLGISSESEN---HSPLYSLAGMAGSVQMFI 246
QY 299 YPNEVLKTRMALR-KTGOY--SGMLDCARRILAREGVAFYKGYVPMGLIIPYAGIDL 354
DB 247 YPVDTLKFRIGQSDLSRGQHSKSIILSNAKELKSVGIRGYGVLTGMFPIKATDL 306
QY 355 AVYETLKNMVLQHYAV-NSADPGVF-----VLLACGMSSTCGQLASYPPLAVRTM 408
DB 307 GTFEGKRTWIGILASRDVNDPODKLPNGLVMAFGALSGSTGATIVFPLNVRTRLQ 366
QY 409 -ASIECAPETMSLSPFHILRTGEGFRLYRGLAPNFKVLPANVISVYVENLKITLGV 466
DB 367 GTSAPHPATYDGFIDCFYKTKNKGFRGLYKGLSPNLKVASVALSYLVENCCKM 425

RESULT 8

T45934

hypothetical protein F5K20.240 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T45934

R;Monfort, A.; Casacuberta, E.; Pujolomech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, January 2000

A;Reference number: Z23017

A;Accession: T45934

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-358 <MON>

A;Cross-references: UNIPROT:Q9M333; EMBL:AL132960

A;Experimental source: cultivar Columbia; BAC clone F5K20

C;Genetics:

A;Map position: 3

A;introns: 98/3; 157/3; 207/3; 234/3; 258/2; 281/1

A;Note: F5K20.240

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 19.6%; Score 476; DB 2; Length 358;
Best Local Similarity 33.4%; Pred. No. 3.9e-25;
Matches 113; Conservative 55; Mismatches 122; Indels 48; Gaps 8;

QY 160 HSTIFVGENLTVPDEFTVERQGMWRL-----LVAGGAGAV 199
DB 25 HNTVAVAGNRKLLQQQ--PQTQOTOSCHQHNKNSLNOQQHFGTVERLLAGIAGAF 82
QY 200 SRTCTAPLRLKYLMOVHNASR-----NNMGIVGFTQMIREGASLWNGINVLK 254
DB 83 SKCTCTAPLRLTLTLFOIQGMSBALISSNINHEMSRIYKESGFRPFMKGILVYVAHRL 142
QY 255 PESAIKFMAYEQIKRLVGS-----QETLRHERLVAGSLAGAIQSSIPMEVLKT 306
DB 143 PYGAVNFVAEEYKTFHNSPVLQSYKGNAGVDISVHFGGLAGLTAAGATVPLDLV 202
QY 307 RMLAKRTQVSGMLDCARRILAREGVAFYKGYVPMGLIIPYAGIDLAVYETLKNM 366

DB 203 RLSDAGVGH-----APRTICREEGILYKGIAGATLLGVGPELSAIPAAVETFKT 256
QY 367 HYAVNSADPGVFVLLACGMSSTCGQLASYPPLAVRTM 408
DB 257 H---RPNDSNAVVSILCGSISGIVSSATFPLDVRHRRQLBGA-GGRARVYTTGL 312
QY 424 KHLRTGAFGLYRGLAPNFKVLPANVISVYVENLK 461
DB 313 KHIFKTEGMKGLYRGLIPEYKVPVGVGIAFMFTFEELK 350

RESULT 9

T47703

Ca-dependent solute carrier-like protein - Arabidopsis thaliana

N;Alternate names: protein F116.50

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: T47703

R;Benes, V.; Wurnbach, E.; Drzonek, H.; Anzorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000

A;Reference number: Z24473

A;Accession: T47703

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-332 <BEN>

A;Cross-references: UNIPROT:Q9M058; EMBL:AL161667

A;Experimental source: cultivar Columbia; BAC clone F116

C;Genetics:

A;Map position: 3

A;introns: 63/3; 122/3; 172/3; 206/3; 230/2; 253/1

A;Note: F116.50

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 19.3%; Score 467.5; DB 2; Length 332;
Best Local Similarity 37.2%; Pred. No. 1.3e-24;
Matches 108; Conservative 52; Mismatches 109; Indels 21; Gaps 7;

QY 190 LVAGGAGAVSRTCTAPLRLKYLMOVHNASRN-----NMGIVGFTQMIREGASL 244
DB 38 LLAGGAGAFSKTCTAPLRLTLFVQGMHTVAALRRPSILHEASRLINEGLKAFWK 97
QY 245 GNGINVLKAPSAIKFMAVEQIKR-----LVGSDQETLRHERL---VAGSLAGAI 236
DB 98 GNLVTIARHLPYSSVNFYAEYEHKKFMVYTGHEHKEGISSNLVHFPVAGGLAGIT 157
QY 297 SIYMEVLKTRMALR-KTGOYSGMLDCARRILAREGVAFYKGYVPMGLIIPYAGIDL 355
DB 158 ATYPLDLVTRLLAQKLVLYSGIMHTLASITTDGILGLYKGLGTTLVGVSIAISFS 217
QY 356 VYETLKNMVLQHYAVNSADPGVFVLLACGMSSTCGQLASYPPLAVRTM 408
DB 218 VVESLNSYV---RSTRPHDSPIMVSLACSLGSIASSTATFPLDVRRRKQLE-GIG 273
QY 416 EYTMSSL---FKHLRTGAFGLYRGLAPNFKVLPANVISVYVENLK 462
DB 274 VVYKTLGLTKRIQTEGARGLYRGLIPEYKVPVGVGICFMTYETLKL 323

RESULT 10

T04273

hypothetical protein F20B18.290 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04273

R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 1999

A;Reference number: Z15263

A;Accession: T04273

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-332 <BEV>

A;Cross-references: UNIPROT:Q9SZ19; EMBL:AL049483

A;Experimental source: cultivar Columbia; BAC clone F20B18

C;Genetics:

Plant Mol. Biol. 41, 687-700, 1999

A>Title: Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1 locus on

A/Reference number: Z24835; MUID:20108326; PMID:10645728

A/Accession: T51158

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-381 <COM>

A/Cross-references: UNIPROT:O65023; EMBL:AF049236; PDB:AA14414.1

C/Genetic:

A/Map position: 3

A/Introns: 116/3; 156/3; 175/3; 203/3; 226/3; 264/2; 321/1; 347/2

Query Match 17.6%; Score 425.5; DB 2; Length 381;

Best Local Similarity 33.3%; Pred. No. 1.2e-21;

Matches 92; Conservative 56; Mismatches 111; Indels 17; Gaps 4;

QY 192 AGGAGAVSRCTAPLDRILVLMQVHA-----SRNNMGIVGFTQMIREGARSIMRG 245

DB 93 AGALAGAACTVAPLDRITLMOHTGIRLGOOSAKKAIFIEATITLAAEEGVKGYWK 152

QY 246 NGINVLKIAPESAIKFMAVEQIKRLVGSDOETLRIHERLVAGSLAGAAOSSITPYMEVLK 305

DB 153 NLQGVIRVLPYSVAQLAYSTYKLPFGKDDLSVIGRLAAGACAGMTSTLLTPLDVLR 212

QY 306 TRNALRRTQYSGMLDCARRILAREGVAAFYKGYVPMGLIIPYAGIDLAVETLKNAML 365

DB 213 LRLAVEP--RYRTMSQVALSMLRDEGIASFYGLGSPVAGIAPVAVNFCIFDLVKSLP 270

QY 366 QHVAANSADPGVAVLACGTMSSSTCGQLASYPALVTRNOQASITGAEVMTSSIFKH 425

DB 271 EERKKAQSSJLRAVLSAGIATLTTC---YPLDVARQWQ---MKGTYSKISPEAFAG 321

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 426 ILRTGAGFLYRGAPFMKVIIPAVSISYVYENLK 461

DB 322 IIRDDGLIGYRGFLPALATLPRSSIRLTTFPMVK 357

QY 191 VAGGAGAVSRCTAPLDRILVLMQVHAS-RSNNMGIVGFTQMIREGARSIMRGIN 249

DB 27 LAGVAVAGAVSRCTAPLDRILVLMQVHAS-RSNNMGIVGFTQMIREGARSIMRGIN 86

QY 250 VLKIAPESAIKFMAVEQIKRLV-----GSDOETLRIHERLVAGSLAGAAOSSITPYMEVL 304

DB 87 CIRIFPYSVAQFVYVYACCKKLPHVNGNNGEQTLTYORLFSALCGGCGVAVTVDL 146

QY 305 KTRMALRKTQYSGMLDCARRILARE-----GVAAPFYKGYVPMGLIIPY 349

DB 147 KTRMALRKTQYSGMLDCARRILARE-----GVAAPFYKGYVPMGLIIPY 205

QY 350 AGIDLAVETLKNAMLQHVANSAD-----PGVFLIACGTMSSSTCGQLASYPALVTR 404

DB 206 VALNFAVYEQLR-----EFGVSSDAPQPSWKSMLYKLTIGALISGVAAQTITPFDLRRR 260

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

QY 405 MQQASIEGAPV--TMSLFFKHIL--RTEGAFGLYRGAPFMKVIIPAVSISYVYE 458

DB 261 FOVLAM--GGNEIGFPTYSVMDLVITIGRAEGVSGYKGLAANLFRVPSTAVSWLVE 317

Search completed: August 5, 2005, 20:30:41

Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 20:24:46 ; Search time 175 Seconds
(without alignments)
1372.372 Million cell updates/sec

Title: US-10-063-565-58
Perfect score: 2423
Sequence: 1 MCLCLYVPIVIGAEQTEFOY.....VSISYVYENKLTIGVQSR 469

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Uniprot_03:*\n1: uniprot_sprot:*\n2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2423	100.0	469	2	06UX48
2	2417	99.8	469	2	06KCM7
3	2360	97.4	469	2	08X3P6
4	2144	88.5	489	2	0705K2
5	2143	88.4	503	2	06KCM6
6	2123	87.6	568	2	096P21
7	2096	86.5	502	2	08BH00
8	2082	85.9	501	2	06NMX8
9	2082	85.9	515	2	06NMX8
10	2075	85.6	514	2	080T78
11	1975	81.5	514	2	07ZVD5
12	1895	78.2	469	2	06NYZ6
13	1866	77.8	366	2	06KCM4
14	1843	76.1	366	2	08VBT4
15	1566	64.6	308	2	09BSA6
16	1556	64.1	477	2	06L4A9
17	1554	64.2	468	2	0705K3
18	1543	63.7	467	2	06GOS1
19	1531.5	63.2	535	2	07Z3A6
20	1514.5	62.5	473	2	07T0U6
21	1501	61.9	477	2	06PUJ9
22	1499	61.9	458	2	0705K4
23	1494	61.7	475	2	018757
24	1494	61.7	477	2	06NUT1
25	1490	61.5	475	2	08BMD8
26	1486	61.3	475	2	07TPC2
27	1469	60.6	384	2	096N04
28	1333	55.0	418	2	086Y43
29	1308	54.0	411	2	09P129
30	1305	53.9	482	2	09BV35
31	1289	53.2	524	2	07PMW8

32	1263	52.1	473	2	09D5G5
33	1245.5	51.4	583	1	09VTX4
34	1177.5	48.6	588	1	CMC3_CABEL
35	1102	45.5	520	2	08NR46
36	1101.5	45.5	565	1	CMC3_CABEL
37	956.5	39.5	363	2	09VTX3
38	846	34.7	515	2	069X19
39	840.5	34.7	312	2	08BVN7
40	835	34.5	232	2	08R225
41	833.5	34.4	466	2	06Z790
42	825	34.0	479	2	09L7Z8
43	823	33.9	478	2	09FLS8
44	822	33.0	208	2	08N2N4
45	806.5	33.3	487	2	09FI43
46	775	32.0	448	2	06DRB4
47	723	29.8	251	2	08NS51
48	679	28.0	232	2	08N7R4
49	614	25.3	166	2	099KD3
50	583	24.1	517	2	06CTN2
51	575.5	23.8	551	2	06C6B6
52	574.5	23.7	519	2	06PP99
53	548	22.6	631	2	09HE62
54	530.5	21.9	493	2	0755U9
55	523	21.6	547	2	06BYB6
56	521	21.5	355	2	061583
57	519	21.4	352	2	004619
58	506	20.9	545	1	CMC1_YEAST
59	502	20.7	540	2	06BYB7
60	502	20.7	545	2	096U51
61	485.5	20.0	365	2	08W4M2
62	479	19.8	426	2	094502
63	476	19.6	358	2	09M333
64	471	19.4	333	2	084J51
65	470	19.4	322	2	09F082
66	467.5	19.3	332	2	09M058
67	462.5	19.1	330	2	08LCH4
68	454	18.7	318	2	086VD7
69	453.5	18.7	332	2	08COK5
70	450.5	18.6	332	2	08N2U1
71	450	18.6	335	2	09S2I9
72	448.5	18.5	330	1	GDC_BOVIN
73	444.5	18.3	337	2	067Z63
74	442.5	18.3	337	2	08L7R0
75	439.5	18.1	331	2	07ZV72
76	437	18.0	318	2	08R0Y8
77	435	18.0	348	2	07XJQ2
78	432	17.8	425	2	06Z782
79	431	17.8	396	2	06E5A5
80	426.5	17.6	332	1	GDC_HUMAN
81	426.5	17.6	358	2	07S563
82	426.5	17.6	358	2	06SKR7
83	425.5	17.6	415	2	065023
84	423.5	17.5	366	2	012251
85	422.5	17.4	316	2	0750J8
86	422	17.4	332	1	GDC_RAT
87	416.5	17.2	381	2	09LDS4
88	415.5	17.1	415	2	08LCT8
89	415.5	17.1	415	2	09M024
90	415.5	17.1	466	1	BT1_MALIZB
91	414.5	17.1	305	2	08IHJ0
92	414.5	17.1	318	2	06RHS3
93	414	17.1	340	2	08S1A3
94	412.5	17.0	385	2	09ZNY4
95	411.5	17.0	302	2	070HR1
96	411	17.0	338	2	06C3A2
97	407	16.8	316	2	09N137
98	405	16.7	290	2	08TMS3
99	405	16.7	355	2	09VUL7
100	403.5	16.7	428	2	09LV81
101	402	16.6	285	2	070EQ1
102	400.5	16.6	419	2	069XJ8
103	388.5	16.0	337	2	06PPR3
104	387	16.0	398	2	06BYS7

09d5g5	mus musculus
09vtx4	drosophila
020799	caenorhabdi
08mr46	drosophila
019529	caenorhabdi
09vtx3	drosophila
069x19	oryza sativ
08bvnt7	mus musculus
08r225	mus musculus
06z790	oryza sativ
09l7z8	arabidopsis
09fls8	arabidopsis
08n2n4	homo sapien
09fi43	arabidopsis
06drb4	brachydanio
08ns51	homo sapien
08n7r4	homo sapien
099kd3	mus musculus
06ctn2	kluyveromyc
06c6b6	yarrowia li
06pp99	candida gla
09he62	neurospora
0755u9	asbya goss
06byb6	debaromyce
061583	oryza sativ
004619	arabidopsis
p482j3	saccharomyc
06byb7	debaromyce
096u51	saccharomyc
08w4m2	arabidopsis
094502	schizosacch
09m333	arabidopsis
084j51	oryza sativ
09f082	oryza sativ
09m058	arabidopsis
08lch4	arabidopsis
086vd7	homo sapien
08cok5	mus musculus
08n2u1	homo sapien
09s2i9	arabidopsis
001888	bos taurus
067z63	arabidopsis
081770	brachydanio
07z72	brachydanio
08r0y8	mus musculus
07xjq2	arabidopsis
06z782	oryza sativ
06e5a5	hordeum vul
p16260	homo sapien
07s563	neurospora
06skr7	oryza sativ
065023	arabidopsis
012251	saccharomyc
0750j8	asbya goss
p16261	ratuus norv
09lds4	oryza sativ
08lct8	arabidopsis
09m024	arabidopsis
p29518	zea mays (m
08ihj0	brachydanio
06rhs3	debaromyce
08s1a3	oryza sativ
09zny4	solanum tub
07gh11	anopheles g
06c3a2	yarrowia li
09n137	trichomonas
08tms3	drosophila
09vul7	drosophila
09lv81	arabidopsis
07geq1	anopheles g
069xj8	oryza sativ
06ppr3	candida gla
06bys7	debaromyce

105	385	15.9	305	2	Q86DE1	Q86de1 trichomonas	178	314	13.0	297	1	ADT3_HUMAN	P12236 homo sapien
106	383.5	15.8	292	2	Q93717	Q93717 caenorhabdi	179	314	13.0	306	2	P91270	P91270 caenorhabdi
107	383.5	15.8	324	2	Q9SUV1	Q9suv1 arbidopsi	180	314	13.0	386	1	ADT1_SOLITU	P25083 solanum tub
108	378	15.6	338	2	Q7RXJ3	Q7rxj3 neurospora	181	313.5	12.9	307	2	Q876G3	Q876G3 saccharomyc
109	375.5	15.5	326	2	Q6H6J3	Q6h6j3 oryza sativ	182	313.5	12.9	363	2	Q8BRM5	Q8BRM5 arbidopsi
110	373.5	15.4	419	2	Q9MA27	Q9ma27 arbidopsi	183	313	12.9	290	2	Q7ZT24	Q7ZT24 rana rugosa
111	373.5	15.4	426	2	Q9MA27	Q9ma27 arbidopsi	184	313	12.9	290	2	Q7ZT24	Q7ZT24 rana rugosa
112	369	15.2	418	2	Q9C9R4	Q9c9r4 arbidopsi	185	313	12.9	290	1	ADT3_BOVIN	P18007 rana rugosa
113	365	15.1	330	2	Q6FN43	Q6fn43 candida gla	186	313	12.9	298	2	ADT3_BOVIN	P32007 bos taurus
114	363	15.0	352	2	Q656X5	Q656x5 oryza sativ	187	313	12.9	298	2	Q9PRH1	Q9prh1 rana rugosa
115	361	14.9	339	2	Q6C1K5	Q6c1k5 yarrowia li	188	313	12.9	326	2	Q8LEZ2	Q8LEZ2 arbidopsi
116	358.5	14.8	333	2	Q9F173	Q9f173 arbidopsi	189	313	12.9	360	2	Q9V551	Q9V551 dirosophila
117	355	14.7	394	2	Q6Z3Q5	Q6z3q5 oryza sativ	190	312.5	12.9	299	2	Q9V551	Q9V551 dirosophila
118	354	14.6	326	1	YE08_SCHPO	Y08schpo schizosacch	191	312.5	12.9	307	1	ADT3_YEAST	P18238 saccharomyc
119	351.5	14.5	335	2	Q8RXZ9	Q8rxz9 arbidopsi	192	312.5	12.9	320	2	ADT3_YEAST	Q921P8 mus musculu
120	351.5	14.5	336	2	Q9LFF7	Q9lff7 arbidopsi	193	312	12.9	298	1	ADT2_BOVIN	Q86b5 bos taurus
121	350	14.4	381	2	Q6CMP3	Q6cmp3 kluyveriomy	194	311	12.8	290	2	Q800B6	Q800B6 rana rugosa
122	349.5	14.4	334	2	Q942Z2	Q942z2 oryza sativ	195	311	12.8	298	2	Q9Y1C4	Q9Y1C4 rana rugosa
123	349	14.4	357	1	LEU5_YEAST	P38702 saccharomyc	196	310	12.8	298	1	ADT2_HUMAN	P05141 homo sapien
124	348	14.4	335	2	Q750M2	Q750m2 ashbya goss	197	310	12.8	298	1	ADT2_MOUSE	P51881 mus musculu
125	344	14.2	317	2	Q8TFH2	Q8tfh2 schizosacch	198	310	12.8	386	2	P93767	P93767 lycopersico
126	337.5	13.9	200	2	Q86DZ9	Q86dz9 schistosoma	199	309	12.8	297	1	ADT1_RABIT	Q46373 coryctolagus
127	336.5	13.9	345	2	Q7Z2B0	Q7z2b0 brachydanio	200	309	12.8	298	1	ADT2_RAT	Q09073 ratus norv
128	335	13.8	308	1	ADT1_CHURE	P27080 chlamydomon	201	309	12.8	298	2	Q21809	Q21809 caenorhabdi
129	334.5	13.8	305	1	ADT1_KLUDI	P49382 kluyveriomy	202	308.5	12.7	308	2	Q8TEA7	Q8TEA7 neocallimas
130	332.5	13.7	304	2	Q875O6	Q875o6 saccharomyc	203	308.5	12.7	308	2	Q7LNP2	Q7LNP2 neocallimas
131	332.5	13.7	385	2	Q6YZM6	Q6yzm6 oryza sativ	204	308.5	12.7	318	1	ADT2_YEAST	P18239 saccharomyc
132	331.5	13.7	346	2	Q8LFX8	Q8lfx8 arbidopsi	205	308.5	12.7	320	2	Q8NBT6	Q8nbt6 homo sapien
133	331.5	13.7	348	2	Q9LJX5	Q9ljx5 arbidopsi	206	308	12.7	298	1	ADT1_MOUSE	P48962 mus musculu
134	331	13.7	382	1	ADT1_ORYSA	P31691 oryza sativ	207	308	12.7	298	2	Q8BVT9	Q8bvt9 mus musculu
135	331	13.7	382	1	ADT1_ORYSA	P31691 oryza sativ	208	308	12.7	298	2	Q8BVT9	Q8bvt9 mus musculu
136	330	13.6	313	1	ADT1_NEUCR	Q6ZGX0 oryza sativ	209	308	12.7	301	2	Q6BENO	Q6bno brachydanio
137	330	13.6	315	2	Q8J0U1	Q8j0u1 gaueunomy	210	308	12.7	320	2	Q80WZ8	Q80WZ8 mus musculu
138	329	13.6	388	2	Q49875	Q49875 lupinus alb	211	308	12.7	781	2	Q9LKMJ6	Q9lmj6 arbidopsi
139	328	13.5	322	1	ADT1_SCHPO	Q09188 schizosacch	212	307	12.7	298	2	Q61P28	Q61P28 xenopus lae
140	328	13.5	341	2	Q8WDT9	Q8wut9 homo sapien	213	307	12.7	298	2	Q91PM9	Q91pm9 xenopus lae
141	327.5	13.5	302	2	Q8J0M2	Q8j0m2 yarrowia li	214	307	12.7	315	2	Q9HOC2	Q9hoc2 homo sapien
142	327.5	13.5	302	2	Q6CH49	Q6ch49 yarrowia li	215	307	12.7	331	1	ADT2_WHEAT	Q41630 triticum ae
143	327.5	13.5	312	2	Q6C129	Q6c129 yarrowia li	216	307	12.7	331	2	Q64731	Q64731 arbidopsi
144	326.5	13.5	305	2	Q9P876	Q9p876 pichia jadi	217	305.5	12.6	304	2	Q25129	Q25129 halocynthia
145	326.5	13.5	310	2	Q8H727	Q8h727 phycopthor	218	305.5	12.6	308	2	Q8NKS7	Q8nks7 neocallimas
146	326.5	13.5	318	2	Q6AYL0	Q6ayl0 ratulus norv	219	305.5	12.6	308	2	Q8NKS7	Q8nks7 neocallimas
147	326	13.5	381	1	ADT1_ARATH	P31167 arbidopsi	220	305.5	12.6	311	2	Q6DG32	Q6dg32 brachydanio
148	325.5	13.4	306	2	Q6FUE0	Q6fue0 candida gla	221	305	12.6	297	1	ADT3_PIG	Q6q9r9 saccharomyc
149	325	13.4	387	2	Q756S0	Q756s0 ashbya goss	222	305	12.6	298	2	Q6PY4	Q6py4 ratulus norv
150	325	13.4	305	1	ADT1_MAIZE	P04709 zea mays (m	223	305	12.6	304	2	Q876G4	Q876G4 saccharomyc
151	324.5	13.4	317	2	Q86PS1	Q86ps1 leishmania	224	305	12.6	361	2	Q8NUT6	Q8nut6 cryptococcu
152	324.5	13.4	318	1	DNC_MOUSE	Q9dams mus musculu	225	305	12.6	377	1	R1M2_YEAST	P38127 saccharomyc
153	324	13.4	216	2	Q43378	Q43378 homo sapien	226	305	12.6	590	2	Q81364	Q81364 piactmodium
154	324	13.4	333	2	Q7S2H8	Q7s2h8 neurospora	227	304.5	12.6	298	1	ADT1_HUMAN	P12235 homo sapien
155	324	13.4	387	1	ADT2_MAIZE	P12857 zea mays	228	304.5	12.6	316	2	Q61ZB5	Q61zb5 cicerutius
156	323.5	13.4	305	2	Q9P875	Q9p875 pichia jadi	229	303	12.5	339	1	ADT1_CHIKE	P31692 chlorella k
157	323.5	13.4	386	1	ADT2_SOLITU	P27081 solanum tub	230	302.5	12.5	301	2	Q8WTR4	Q8wtr4 euploies sp
158	323	13.3	366	1	ADT1_GOSHI	Q22342 gossypium h	231	302.5	12.5	310	2	Q9AWN4	Q9awn4 oryza sativ
159	322.5	13.3	305	2	Q6C9U8	Q6c9u8 yarrowia li	232	302.5	12.5	318	2	Q6AVS9	Q6avs9 oryza sativ
160	322.5	13.3	305	2	Q9P8M1	Q9p8m1 yarrowia li	233	302.5	12.5	320	1	DNC_HUMAN	Q9hc21 homo sapien
161	322.5	13.3	306	2	P78754	P78754 schizosacch	234	302.5	12.5	337	2	Q7OIC6	Q7oic6 anopheles g
162	322	13.3	309	1	ADT1_YEAST	P04710 saccharomyc	235	302	12.5	298	2	Q8AYM3	Q8aym3 gallus gall
163	321	13.2	311	1	ADT1_WHEAT	Q41629 triticum ae	236	302	12.5	299	2	Q95YX4	Q95yx4 ethmoestigm
164	321	13.2	379	2	Q49447	Q49447 arbidopsi	237	301.5	12.4	311	2	Q96C01	Q96c01 homo sapien
165	320.5	13.2	308	2	Q875W6	Q875w6 saccharomyc	238	301.5	12.4	316	1	MFTC_MOUSE	Q8bm98 mus musculu
166	319	13.2	303	2	Q74260	Q74260 candida par	239	301.5	12.4	316	2	Q8KOB7	Q8kob7 mus musculu
167	318.5	13.1	318	2	Q80XJ6	Q80xj6 mus musculu	240	301	12.4	301	2	Q8BEP1	Q8bep1 anopheles g
168	318	13.1	241	2	Q86ER7	Q86er7 schistosoma	241	301	12.4	365	1	Q6BMW3	Q6bmw3 debaryomyce
169	317.5	13.1	317	2	Q875W7	Q875w7 saccharomyc	242	300.5	12.4	315	2	MFTC_MACFA	Q95175 maccia faac
170	317.5	13.1	315	2	Q9N647	Q9n647 leishmania	243	300.5	12.4	330	2	Q6BWR5	Q6bwr5 debaryomyce
171	316.5	13.1	385	1	ADT2_ARATH	P40941 arabidopsi	244	300	12.4	298	2	ADT1_RAT	Q05362 ratulus norv
172	316	13.0	313	2	Q44967	Q44967 caenorhabdi	245	300	12.4	298	1	Q6PBFS	Q6pbfs xenopus tro
173	316	13.0	323	2	Q6NVC0	Q6nvc0 homo sapien	246	300	12.4	331	2	Q8LEH2	Q8leh2 arbidopsi
174	316	13.0	331	2	Q41628	Q41628 triticum tu	247	299.5	12.4	289	2	Q82049	Q82049 ribes nigru
175	316	13.0	379	2	Q8L9Y1	Q8l9y1 arabidopsi	248	299.5	12.4	311	2	Q922G0	Q922g0 m triken cdm
176	315.5	13.0	293	2	Q756A1	Q756a1 ashbya goss	249	299.5	12.4	315	1	MFTC_HUMAN	Q9h2d1 homo sapien
177	314.5	13.0	322	2	Q6Z292	Q6z292 brassica ol	250	299	12.3	300	2	Q86PT7	Q86pt7 manduca sex

251	299	12.3	301	2	081J34	081J34 plasmidium	324	275.5	11.4	307	2	06FTE5	06fetes candida gla
252	299	12.3	307	2	0709G0	07g90 anopheles g	325	275.5	11.4	348	2	06FRJ5	06frj5 candida gla
253	299	12.3	376	2	09FR77	09fr77 arabadopsis	326	275.5	11.4	365	2	09GPR5	09gpr5 dictyosteli
254	298.5	12.3	308	2	07XA87	07xa87 arabadopsis	327	275	11.3	319	2	06CJ10	06cj10 yarrowia li
255	298	12.3	300	2	086Pg2	086pg2 bombyx mori	328	275	11.3	362	2	075IL2	075il2 ashbya gos
256	298	12.3	301	2	025692	025692 plasmidium	329	275	11.3	373	1	YIA6 YEAST	P40556 saccharomy
257	298	12.3	303	2	09VTM8	09vtm8 dictyostella	330	274.5	11.3	254	2	08BK05	08bk05 mus musculu
258	297.5	12.3	301	2	086AV5	086av5 dictyosteli	331	274.5	11.3	336	2	06C107	06c107 yarrowia li
259	297	12.3	297	1	ADT1 BOVIN	P02722 bos taurus	332	274	11.3	300	2	001813	001813 caenorhabdi
260	297	12.3	361	2	09PE17	09pe17 echinosacch	333	274	11.3	303	2	014281	014281 echinosacch
261	296.5	12.2	291	2	08LB08	08lb08 arabadopsis	334	274	11.3	335	1	YEA6 YEAST	P39953 saccharomy
262	296.5	12.2	315	2	09BE05	09be05 macaca fasc	335	274	11.3	381	2	06FJm1	06fjml candida gla
263	296.5	12.2	330	2	07QJ77	07qj77 anopheles g	336	273.5	11.3	277	2	013660	013660 schizosacch
264	296	12.2	298	2	06NX10	06nx10 brachydanio	337	273.5	11.3	341	2	06DFK2	06dfk2 xenopus lae
265	296	12.2	298	2	06P7N0	06p7n0 xenopus tro	338	273.5	11.3	677	1	CMC1 MOUSE	06bhf9 mus musculu
266	296	12.2	309	2	097470	097470 dictyosteli	339	272.5	11.2	317	2	06COP3	06cqp3 kluyveromyc
267	295.5	12.2	299	1	ADT1_DROME	026365 drosophila	340	272	11.2	361	2	06C2S7	06c2s7 yarrowia li
268	295.5	12.2	307	2	062526	062526 drosophila	341	271.5	11.2	291	2	06GQ22	06gq22 xenopus lae
269	295.5	12.2	312	2	08IRAO	08irao drosophila	342	271.5	11.2	314	2	06B1H1	06b1h1 saccharomyc
270	295.5	12.2	361	2	06FPQ2	06fpq2 candida gla	343	271.5	11.2	350	2	07PZC5	07pzc5 anopheles g
271	295	12.2	301	2	026006	026006 plasmidium	344	271	11.2	304	2	098T90	098t90 eupetromena
272	295	12.2	310	2	09NVN5	09nvns homo sapien	345	270.5	11.2	300	2	045865	045865 caenorhabdi
273	294.5	12.2	355	2	09VOJ7	09voj7 drosophila	346	270.5	11.2	315	2	06P4X8	06p4x8 xenopus tro
274	294.5	12.2	430	2	076KG1	076kg1 penicillium	347	270.5	11.2	678	2	CMC1_HUMAN	075746 homo sapien
275	293.5	12.1	305	2	06CLG4	06clg4 kluyveromyc	348	270.5	11.2	678	2	096AM8	096am8 homo sapien
276	293.5	12.1	312	2	022261	022261 arabadopsis	349	269.5	11.1	341	2	06P316	06p316 xenopus tro
277	293	12.1	306	2	018683	018683 caenorhabdi	350	269	11.1	324	2	001883	001883 caenorhabdi
278	292.5	12.1	318	2	09BUJ6	09buj6 toxoplasma	351	269	11.1	379	2	09VAV3	09vav3 drosophila
279	292	12.1	301	1	ADT1_AMOGA	027238 anopheles g	352	269	11.1	706	2	09C2K1	09c2k1 neurospora
280	292	12.1	317	2	091336	091336 rana sylvat	353	268.5	11.1	676	2	06PCF1	06pcf1 xenopus lae
281	291.5	12.0	300	2	06VOF3	06vof3 arabadopsis	354	268	11.1	317	2	06CDS3	06cds3 yarrowia li
282	291	12.0	300	2	06V013	06v013 apis mellif	355	268	11.1	365	2	0758L4	0758l4 ashbya gos
283	290.5	12.0	300	2	09FNM6	09fnm6 arabadopsis	356	267.5	11.0	307	2	09XM22	09xm22 ascaris suu
284	289.5	11.9	300	2	09NHW5	09nhw5 lucilia cup	357	267	11.0	307	2	090X50	090x50 melegria g
285	289.5	11.9	307	2	076286	076286 trypanosoma	358	267	11.0	450	2	0871K0	0871k0 neurospora
286	289	11.9	304	2	095T49	095t49 drosophila	359	266.5	11.0	317	2	075EP3	075ep3 ashbya gos
287	288.5	11.9	239	2	09ASP6	09asf6 cryza sativ	360	265.5	10.9	291	2	08HXP3	08hxp3 macaca fasc
288	288.5	11.9	307	2	026697	026697 trypanosoma	361	265	10.9	307	2	09DD77	09dd77 gallus gall
289	288.5	11.9	311	2	075B11	075b11 ashbya gos	362	265	10.9	676	2	06IND0	06ind0 xenopus lae
290	288	11.9	295	2	07PGF7	07pgf7 anopheles g	363	264.5	10.9	306	2	06CSN9	06csn9 yarrowia li
291	288	11.9	301	2	07RHV1	07rhv1 plasmidium	364	264	10.9	359	2	078XW0	078xw0 brachydanio
292	288	11.9	305	2	07PGF6	07pgf6 anopheles g	365	264	10.9	618	2	06ESH9	06esh9 cryza sativ
293	287.5	11.9	379	2	075AC6	075ac6 ashbya gos	366	263	10.9	304	1	MR54 YEAST	P23500 ashbya gos
294	287	11.8	286	2	07ZVV6	07zvv6 brachydanio	367	262	10.8	307	2	08AYM4	08aym4 gallus gall
295	287	11.8	315	2	086ZL1	086zl1 podospora a	368	262	10.8	404	2	06CGR5	06cgr5 yarrowia li
296	286.5	11.8	321	2	09BSK2	09bsk2 homo sapien	369	261.5	10.8	300	2	017407	017407 caenorhabdi
297	286.5	11.8	353	2	08CJ24	08cj24 mus musculu	370	261.5	10.8	675	1	CMC2_HUMAN	09uj80 homo sapien
298	286.5	11.8	356	2	08CJ23	08cj23 mus musculu	371	261.5	10.8	702	1	CMC1_CABEL	021153 caenorhabdi
299	286	11.8	305	2	08MVR7	08mvr7 myctotherus	372	261	10.8	361	2	0755I0	0755i0 ashbya gos
300	286	11.8	308	2	08MVR8	08mvr8 myctotherus	373	261	10.8	675	2	08C140	08c140 mus musculu
301	286	11.8	325	1	UCP5_HUMAN	095258 homo sapien	374	261	10.8	682	2	06PFM3	06pfm3 brachydanio
302	285	11.8	355	1	UCP5_MOUSE	092252 mus musculu	375	260.5	10.8	341	2	08K4J8	08k4j8 mus musculu
303	284.5	11.7	298	2	06WRX4	06wrx4 brachyosco	376	260.5	10.8	364	2	08R0Z5	08r0z5 mus musculu
304	284.5	11.7	318	2	06BHC4	06bhc4 debaryomyce	377	260	10.7	334	2	06MFR0	06mfr0 neurospora
305	284	11.7	306	2	08MVR5	08mvr5 myctotherus	378	260	10.7	337	2	07SAV0	07sav0 neurospora
306	284	11.7	308	2	08MVR6	08mvr6 myctotherus	379	260	10.7	576	2	08ID23	08id23 plasmidium
307	284	11.7	310	2	07S4D6	07s4d6 neurospora	380	260	10.7	674	2	08HKW2	08hkx2 macaca fasc
308	284	11.7	342	2	07QIES	07qies anopheles g	381	259.5	10.7	311	1	UCP3_BOVIN	077732 bos taurus
309	283.5	11.7	368	2	06CM21	06cm21 kluyveromyc	382	259.5	10.7	380	2	09NHV6	09nhv6 drosophila
310	282	11.6	322	2	09JMH0	09jmh0 rattus norv	383	259	10.7	308	1	UCP3_PIG	097649 sus scrofa
311	282	11.6	325	2	09EP88	09ep88 rattus norv	384	259	10.7	311	1	FLX1_YEAST	P40464 saccharomyc
312	281.5	11.6	371	2	09UTD6	09utd6 schizosacch	385	259	10.7	685	1	CMC1_DROME	09va73 drosophila
313	280.5	11.6	307	2	06CJ97	06cj97 kluyveromyc	386	258.5	10.7	236	2	07XAT3	07xat3 cryza sativ
314	280.5	11.6	314	2	06P036	06p036 brachydanio	387	258.5	10.7	236	2	09AVL2	09av12 cryza sativ
315	280	11.6	322	1	SFC1_YEAST	P33303 saccharomyc	388	258.5	10.7	297	2	06FMG4	06fmg4 candida gla
316	279	11.5	344	2	07ZUN1	07zun1 brachydanio	389	258.5	10.7	304	2	070605	07q605 anopheles g
317	278.5	11.5	291	2	09CR58	09cr58 m mus muscu	390	258.5	10.7	353	2	06DHC3	06dhc3 brachydanio
318	278	11.5	298	2	044093	044093 drosophila	391	258.5	10.7	676	1	CMC2_MOUSE	09gxx4 mus musculu
319	277.5	11.5	313	2	P91410	P91410 caenorhabdi	392	258	10.6	300	2	093540	093540 caenorhabdi
320	277.5	11.5	313	2	Q21103	Q21103 caenorhabdi	393	258	10.6	305	2	06FL69	06fl69 candida gla
321	277.5	11.5	314	1	YG20 YEAST	P53257 saccharomyc	394	258	10.6	307	2	077304	077304 oxytricha f
322	276.5	11.4	731	2	070I16	070i16 anopheles g	395	256.5	10.6	280	2	06BPM0	06bpm0 debaryomyce
323	276	11.4	288	2	044094	044094 drosophila	396	256.5	10.6	305	2	09X174	09x174 arabadopsis

397	256	10.6	312	2	Q6BR81	Q6BR81 pachycara b	470	238	9.8	301	2	Q7TPE6	Q7TPE6 mus musculu
398	255	10.5	314	2	Q8BGF9	Q8BGF9 m mus muscu	471	238	9.8	314	2	Q9VZD9	Q9VZD9 drosophila
399	255	10.5	333	2	Q7TSG9	Q7TSG9 mus musculu	472	237.5	9.8	266	2	Q641C8	Q641C8 xenopus lae
400	255	10.5	407	2	Q7PX99	Q7PX99 anopheles g	473	237.5	9.8	310	1	UCP2_BRARE	Q9W720 brachydanio
401	254.5	10.5	252	2	Q9AYT6	Q9AYT6 picea abies	474	237.5	9.8	310	2	Q6UX65	Q6UX65 leuciscus c
402	254.5	10.5	377	2	Q9C910	Q9C910 arbidopsiis	475	237.5	9.8	323	2	Q9W0Y9	Q9W0Y9 drosophila
403	254	10.5	314	2	Q96H78	Q96H78 homo sapien	476	237	9.8	309	2	Q6RZX3	Q6RZX3 dicostonyx
404	254	10.5	314	2	Q95034	Q95034 homo sapien	477	237	9.8	309	2	Q920G8	Q920G8 mus musculu
405	254	10.5	418	2	Q7PM06	Q7PM06 anopheles g	478	236.5	9.8	303	2	Q94638	Q94638 onchocerca
406	253.5	10.5	344	2	Q96A46	Q96A46 homo sapien	479	236.5	9.8	307	2	Q6P4L5	Q6P4L5 xenopus tro
407	253.5	10.5	389	2	Q86VX5	Q86VX5 homo sapien	480	236.5	9.8	322	2	Q9AX03	Q9AX03 oryza sativ
408	253	10.4	279	2	Q6CB90	Q6CB90 yarrowia ll	481	236	9.7	301	1	MCAT_MOUSE	Q9XZ26 mus musculu
409	253	10.4	312	2	Q6BR80	Q6BR80 zoarcetes viv	482	236	9.7	301	1	Q66HP8	Q66HP8 rattus norv
410	253	10.4	336	2	Q6CN42	Q6CN42 kluyveromyc	483	236	9.7	302	1	YDIX_SCHPO	Q10248 schizosacch
411	252	10.4	391	2	Q7S854	Q7S854 homo sapien	484	236	9.7	306	1	CACL_MOUSE	Q8B103 mus musculu
412	251	10.4	314	1	MRS3_YEAST	P10566 saccharomyc	485	236	9.7	312	1	UCP3_HUMAN	P55916 homo sapien
413	250.5	10.3	311	2	Q6R132	Q6R132 antechinus	486	236	9.7	315	2	Q7T3F5	Q7T3F5 brachydanio
414	250.5	10.3	333	2	Q6BDU1	Q6BDU1 debaryomyc	487	235.5	9.7	313	2	Q6AX17	Q6AX17 xenopus lae
415	250	10.3	188	2	Q6CS36	Q6CS36 kluyveromyc	488	235	9.7	309	2	Q9W038	Q9W038 arbidopsiis
416	250	10.3	313	2	Q6TLF4	Q6TLF4 brachydanio	489	235	9.7	374	2	Q6FTW4	Q6FTW4 candida gla
417	250	10.3	364	2	Q6GYH1	Q6GYH1 arbidopsiis	490	235	9.7	906	2	Q6CND4	Q6CND4 kluyveromyc
418	249.5	10.3	314	2	Q94370	Q94370 schizosacch	491	234.5	9.7	312	2	Q23125	Q23125 caenorhabd1
419	249.5	10.3	325	2	Q7QJH5	Q7QJH5 anopheles g	492	234.5	9.7	321	2	Q9VGF7	Q9VGF7 drosophila
420	249	10.3	310	2	Q7YRF3	Q7YRF3 antechinus	493	234.5	9.7	409	2	Q91YK1	Q91YK1 mus musculu
421	248.5	10.3	376	2	Q7QGF5	Q7QGF5 anopheles g	494	234	9.7	308	2	Q7XTC8	Q7XTC8 oryza sativ
422	248.5	10.3	431	2	Q6COV1	Q6COV1 kluyveromyc	495	233.5	9.6	289	2	Q8N9L5	Q8N9L5 homo sapien
423	248	10.2	309	1	UCP2_PIG	Q97562 sus scrofa	496	233.5	9.6	301	2	Q94634	Q94634 onchocerca
424	247.5	10.2	288	2	Q6L4I8	Q6L4I8 oryza sativ	497	233.5	9.6	323	1	GHCI_HUMAN	Q9H336 homo sapien
425	247.5	10.2	307	2	Q7ZXN1	Q7ZXN1 xenopus lae	498	233.5	9.6	343	2	Q7Q1W3	Q7Q1W3 anopheles g
426	247.5	10.2	727	2	Q6BU21	Q6BU21 debaryomyc	499	233.5	9.6	359	1	CG68_HUMAN	Q9B714 homo sapien
427	247	10.2	309	1	UCP2_MOUSE	P70406 mus musculu	500	233	9.6	271	1	PETH_ASHGO	Q60029 ashya goss
428	247	10.2	309	2	Q9ER17	Q9ER17 phodopus su	501	233	9.6	282	2	Q7P1I0	Q7P1I0 anopheles g
429	247	10.2	344	2	Q9R246	Q9R246 mus musculu	502	233	9.6	295	2	Q8LAN8	Q8LAN8 arbidopsiis
430	247	10.2	309	2	Q754D9	Q754D9 ashya goss	503	232.5	9.6	311	2	Q9CEK8	Q9CEK8 arbidopsiis
431	247	10.2	449	2	Q9VT05	Q9VT05 drosophila	504	232.5	9.6	330	2	Q7RRJ2	Q7RRJ2 neurospora
432	247	10.2	497	2	Q7RSC07	Q7RSC07 plasmodium	505	232	9.6	319	2	Q9HEB3	Q9HEB3 neurospora
433	246	10.2	338	2	Q94576	Q94576 schizosacch	506	232	9.6	919	2	Q6FW66	Q6FW66 candida gla
434	245.5	10.1	300	1	MCAT_ARATH	Q93XN7 arbidopsiis	507	231.5	9.6	313	2	Q7QD37	Q7QD37 anopheles g
435	245.5	10.1	307	2	Q6NS20	Q6NS20 xenopus lae	508	231	9.5	296	2	Q21084	Q21084 caenorhabd1
436	245.5	10.1	309	2	Q6TGS8	Q6TGS8 brachydanio	509	231	9.5	308	1	UCP3_MOUSE	P56501 mus musculu
437	245.5	10.1	310	2	Q9FK00	Q9FK00 arbidopsiis	510	230.5	9.5	317	2	Q66PX5	Q66PX5 saccharum o
438	245.5	10.1	325	2	Q94AG6	Q94AG6 arbidopsiis	511	230.5	9.5	317	2	Q6P4S3	Q6P4S3 xenopus lae
439	245	10.1	351	2	Q6C165	Q6C165 yarrowia ll	512	230.5	9.5	338	2	Q9UHR1	Q9UHR1 homo sapien
440	245	10.1	328	2	Q9HB96	Q9HB96 neurospora	513	230	9.5	301	1	MCAT_RAT	P97521 rattus norv
441	244.5	10.1	311	1	UCP3_CANFA	Q9N219 canis famli	514	229.5	9.5	412	2	Q9FHX2	Q9FHX2 arbidopsiis
442	244.5	10.1	332	2	Q9VGD9	Q9VGD9 drosophila	515	229.5	9.5	289	2	Q6FSP4	Q6FSP4 candida gla
443	244.5	10.1	337	2	Q8BGP6	Q8BGP6 m mus muscu	516	229.5	9.5	311	2	Q8SXB4	Q8SXB4 drosophila
444	244.5	10.1	337	2	Q8BX78	Q8BX78 mus musculu	517	229.5	9.5	311	2	Q9VZ93	Q9VZ93 drosophila
445	244.5	10.1	823	2	Q8VZP7	Q8VZP7 arbidopsiis	518	229.5	9.5	313	2	Q66UC1	Q66UC1 oryza sativ
446	244	10.1	309	1	UCP2_RAT	P56500 rattus norv	519	229.5	9.5	360	2	Q8LHE2	Q8LHE2 oryza sativ
447	244	10.1	309	2	Q8CBT0	Q8CBT0 mus musculu	520	229	9.5	306	1	COLT_DROME	Q9V994 drosophila
448	244	10.1	912	2	Q75AH6	Q75AH6 ashya goss	521	229	9.5	307	1	ODC3_YEAST	Q99297 saccharomyc
449	243.5	10.0	309	2	Q7ZVP4	Q7ZVP4 brachydanio	522	229	9.5	344	2	Q9UIC8	Q9UIC8 leishmania
450	243.5	10.0	376	2	Q7T292	Q7T292 brachydanio	523	228.5	9.4	227	2	Q875W5	Q875W5 saccharomyc
451	242.5	10.0	310	2	Q6P013	Q6P013 brachydanio	524	228.5	9.4	238	2	Q6CVF0	Q6CVF0 drosophila
452	242	10.0	303	1	CACL_HUMAN	Q9N873 homo sapien	525	228.5	9.4	305	2	Q6CVF5	Q6CVF5 kluyveromyc
453	242	10.0	306	2	P90932	P90932 caenorhabd1	526	228	9.4	298	2	Q8BY72	Q8BY72 mus musculu
454	242	10.0	309	1	UCP2_CANFA	Q9N211 canis famli	527	228	9.4	298	2	Q8BZ09	Q8BZ09 mus musculu
455	242	10.0	309	1	UCP2_HUMAN	P55851 homo sapien	528	228	9.4	312	2	Q7TMY4	Q7TMY4 dicostonyx
456	242	10.0	345	2	Q9CYJ1	Q9CYJ1 mus musculu	529	228	9.4	319	2	Q6H3X4	Q6H3X4 xenopus lae
457	241.5	10.0	337	2	Q7PLZ5	Q7PLZ5 anopheles g	530	228	9.4	327	2	Q9LRF4	Q9LRF4 arbidopsiis
458	241.5	10.0	364	2	Q6CRD8	Q6CRD8 kluyveromyc	531	227.5	9.4	274	2	Q7YRF2	Q7YRF2 smitthopsiis
459	241.5	10.0	426	2	Q7Q365	Q7Q365 anopheles g	532	227.5	9.4	313	2	Q6DFD6	Q6DFD6 xenopus lae
460	240.5	9.9	284	2	Q6YVE7	Q6YVE7 oryza sativ	533	227	9.4	308	1	UCP3_RAT	P56499 rattus norv
461	240.5	9.9	310	1	UCP2_CYPCA	Q9W755 cyptinus ca	534	226.5	9.3	323	1	GHCI_MOUSE	Q9D663 mus musculu
462	240.5	9.9	902	2	Q12482	Q12482 saccharomyc	535	226.5	9.3	335	2	Q6GNM8	Q6GNM8 xenopus lae
463	239.5	9.9	368	2	Q6FTZ1	Q6FTZ1 candida gla	536	226	9.3	340	1	MPCP_CAEEL	P40614 caenorhabd1
464	239	9.9	314	2	Q81G56	Q81G56 drosophila	537	226	9.3	356	2	Q6GP92	Q6GP92 xenopus lae
465	239	9.9	338	2	Q66H23	Q66H23 rattus norv	538	225.5	9.3	321	2	Q6YX13	Q6YX13 oryza sativ
466	239	9.9	660	2	Q6C7R0	Q6C7R0 yarrowia ll	539	225.5	9.3	368	2	Q6BH17	Q6BH17 debaryomyc
467	239	9.9	844	2	Q9S770	Q9S770 arbidopsiis	540	224.5	9.3	296	2	Q9CA93	Q9CA93 arbidopsiis
468	238.5	9.8	269	2	Q6GLA2	Q6GLA2 xenopus tro	541	224.5	9.3	297	2	Q6CAH9	Q6CAH9 yarrowia ll
469	238.5	9.8	338	2	Q8TBP6	Q8TBP6 homo sapien	542	224.5	9.3	354	2	Q7Q4Q1	Q7Q4Q1 anopheles g

543	223.5	9.2	310	2	08S4C4	08S4C4 zea mays (m	616	212	8.7	301	2	09VZ94	09VZ94 drosophila
544	223.5	9.2	317	2	07K600	07K600 drosophila	617	212	8.7	309	2	066PX6	066PX6 saccharum o
545	223	9.2	320	2	06C4B3	06C4B3 yarrowia li	618	212	8.7	309	2	07X646	07X646 arabisdopsis
546	223	9.2	300	2	06P5K6	06P5K6 brachydanio	619	212	8.7	313	2	094K32	094K32 arabisdopsis
547	223	9.2	305	2	09ZM61	09ZM61 arabisdopsis	620	212	8.7	366	1	YG5F YEAST	P53J30 saccharomyc
548	222.5	9.2	282	2	06C3B4	06C3B4 yarrowia li	621	211.5	8.7	308	2	0755R8	0755R8 ashbya goss
549	222.5	9.2	288	2	09P3T7	09P3T7 schizosacch	622	211.5	8.7	329	2	076P23	076P23 dictyosteli
550	222.5	9.2	301	2	06XU10	06XU10 homo sapien	623	211	8.7	301	1	MCAT_HUMAN	043772 homo sapien
551	222	9.2	289	2	09ER16	09ER16 photodopus su	624	210.5	8.7	312	1	GHG2_MOUSE	09dB41 mus musculu
552	222	9.2	301	2	07ZTP9	07ZTP9 xenopus lae	625	210.5	8.7	360	1	Y051_CABEL	09V461 drosophila
553	222	9.2	356	2	09VUP1	09VUP1 drosophila	626	210	8.7	302	2	09VVS1	043808 homo sapien
554	221.5	9.1	273	2	09XSB1	09XSB1 bos taurus	627	210	8.7	307	1	PM34_HUMAN	061G89 brachydanio
555	221.5	9.1	316	2	07XB4	07XB4 oryza sativ	628	210	8.7	308	2	0610B9	09EPH7 rattus norv
556	221.5	9.1	316	2	09AY13	09AY13 oryza sativ	629	210	8.7	322	2	09EPH7	07SCR2 neurospora
557	221.5	9.1	366	2	06BQ70	06BQ70 debaryomyc	630	210	8.7	488	2	07SCR2	07BSC2 neurospora
558	221	9.1	263	2	06V9R7	06V9R7 homo sapien	631	209.5	8.6	304	2	09NWX2	09NW42 homo sapien
559	221	9.1	305	2	09W2T2	09W2T2 drosophila	632	209	8.6	284	2	094071	094071 candida alb
560	221	9.1	313	2	08LDP6	08LDP6 arabisdopsis	633	209	8.6	306	2	065623	065623 arabisdopsis
561	221	9.1	313	2	09SJY5	09SJY5 arabisdopsis	634	209	8.6	309	2	06NTJ5	06NTJ5 xenopus lae
562	221	9.1	368	1	YM39 YEAST	093J29 saccharomyc	635	209	8.6	313	1	M2OM_BOVIN	P22J22 bos taurus
563	221	9.1	459	2	07KV08	07KV08 drosophila	636	209	8.6	334	2	07QBE3	07QBE3 anophelis g
564	220.5	9.1	183	2	09MZY4	09MZY4 macaca fasc	637	209	8.6	355	2	024451	024451 chlamydomon
565	220.5	9.1	296	2	0750M1	0750M1 ashbya goss	638	209	8.6	359	2	07QAQ2	07QAQ2 anophelis g
566	220.5	9.1	304	2	06C613	06C613 yarrowia li	639	208.5	8.6	232	2	086CZ0	086CZ0 helicoverpa
567	220.5	9.1	306	1	UCPI_RAT	P04633 rattus norv	640	208.5	8.6	289	2	075CE7	075CE7 ashbya goss
568	220	9.1	320	2	06CFT5	06CFT5 yarrowia li	641	208.5	8.6	301	1	ORT1_HUMAN	09Y619 homo sapien
569	219.5	9.1	307	1	UCPI_HUMAN	P25874 homo sapien	642	208.5	8.6	311	1	TXTP_RAT	P32089 rattus norv
570	219.5	9.1	317	1	MPCP YEAST	P23641 saccharomyc	643	208	8.6	302	2	06DE75	06DE75 xenopus lae
571	219.5	9.1	323	1	UCP4_HUMAN	095847 homo sapien	644	208	8.6	338	2	0861R1	0861R1 dictyosteli
572	219.5	9.1	325	2	066PX3	066PX3 saccharum o	645	208	8.6	356	2	06NMJ7	06NMJ7 brachydanio
573	219.5	9.0	356	2	09XZB4	09XZB4 drosophila	646	207.5	8.6	152	2	08RW16	08RW16 arabisdopsis
574	218.5	9.0	359	2	09D8X8	09D8X8 mus muscu	647	207.5	8.6	304	2	096DW6	096DW6 homo sapien
575	218.5	9.0	344	2	027244	027244 caenorhabdi	648	207.5	8.6	355	2	06PC47	06PC47 brachydanio
576	218	9.0	290	2	06BNQ4	06BNQ4 debaryomyc	649	207.5	8.6	358	2	024450	024450 chlamydomon
577	218	9.0	306	2	081845	081845 arabisdopsis	650	207.5	8.6	360	2	08UJ63	08UJ63 rana sylvat
578	218	9.0	309	2	020847	020847 caenorhabdi	651	207	8.5	269	2	018934	018934 caenorhabdi
579	218	9.0	334	2	06GL13	06GL13 xenopus tro	652	207	8.5	302	2	06DJ08	06DJ08 xenopus tro
580	217.5	9.0	306	2	09V3T2	09V3T2 drosophila	653	207	8.5	310	2	09DDA8	09DDA8 xenopus lae
581	217.5	9.0	330	2	09SVB2	09SVB2 arabisdopsis	654	206.5	8.5	293	2	09AVG2	09AVG2 oryza sativ
582	217	9.0	299	2	06CGA2	06CGA2 yarrowia li	655	206.5	8.5	307	2	09ER18	09ER18 photodopus su
583	217	9.0	301	2	08HX12	08HX12 macaca fasc	656	206.5	8.5	311	2	08JZU2	08JZU2 mus musculu
584	217	9.0	301	2	06P6Z8	06P6Z8 xenopus tro	657	206.5	8.5	312	1	DIPL_CABEL	027227 caenorhabdi
585	217	9.0	331	2	066PX4	066PX4 saccharum o	658	206.5	8.5	362	1	MPCP_HUMAN	000335 homo sapien
586	216.5	8.9	236	2	08LB35	08LB35 arabisdopsis	659	206	8.5	290	2	027322	027322 caenorhabdi
587	216.5	8.9	309	2	09GMZ1	09GMZ1 canis famli	660	206	8.5	293	2	074423	074423 ashbya goss
588	216	8.9	301	2	07QAU4	07QAU4 anophelis g	661	205.5	8.5	311	1	TXTP_BOVIN	P79110 bos taurus
589	216	8.9	306	1	UCPI_RABIT	P14271 oryctolagus	662	205.5	8.5	334	1	017970	017970 caenorhabdi
590	215.5	8.9	307	2	06FUM0	06FUM0 candida gla	663	205	8.5	274	2	070HM3	070HM3 homo sapien
591	215.5	8.9	315	1	GHG2_HUMAN	09H1K4 homo sapien	664	205	8.5	281	2	0754C4	0754C4 ashbya goss
592	215.5	8.9	367	2	09VWG0	09VWG0 drosophila	665	205	8.5	286	2	09FX06	09FX06 triticum ae
593	215	8.9	300	2	09AVG1	09AVG1 oryza sativ	666	205	8.5	312	1	TXTP_CABEL	P34519 caenorhabdi
594	215	8.9	315	2	0754C3	0754C3 ashbya goss	667	205	8.5	312	2	06BZ03	06BZ03 debaryomyc
595	215	8.9	329	2	07ZTT6	07ZTT6 brachydanio	668	205	8.5	313	1	M2OM_MOUSE	09CR12 mus musculu
596	215	8.9	347	2	07PZ09	07PZ09 anophelis g	669	205	8.5	356	2	07ZV45	07ZV45 brachydanio
597	214.5	8.9	301	1	ORT1_MOUSE	09W4V5 mus musculu	670	205	8.5	359	2	06RGY3	06RGY3 brachydanio
598	214.5	8.9	301	1	ORT2_HUMAN	09BX12 homo sapien	671	205	8.5	359	2	07ZTU1	07ZTU1 xenopus lae
599	214.5	8.9	311	2	084UC7	084UC7 arabisdopsis	672	205	8.5	361	2	08RY40	08RY40 arabisdopsis
600	214.5	8.9	340	2	09VX14	09VX14 drosophila	673	205	8.5	376	2	07ZTN7	07ZTN7 homo sapien
601	214	8.8	274	2	08JZT2	08JZT2 mus musculu	674	204.5	8.4	298	2	07P823	07P823 anophelis g
602	214	8.8	313	2	09SBS2	09SBS2 arabisdopsis	675	204.5	8.4	303	2	09SKC6	09SKC6 macaca fasc
603	214	8.8	366	2	06CKX9	06CKX9 kluyveromyc	676	204	8.4	307	1	PM34_MOUSE	070519 mus musculu
604	213.5	8.8	281	2	06FZC9	06FZC9 solanum dem	677	204	8.4	317	2	09VAA9	09VAA9 drosophila
605	213.5	8.8	288	2	08CFU7	08CFU7 mus musculu	678	204	8.4	339	2	07R2P8	07R2P8 neurospora
606	213.5	8.8	294	2	08VBZ7	08VBZ7 mus musculu	679	203.5	8.4	312	2	07RS97	07RS97 neurospora
607	213.5	8.8	306	1	UCPI_MESAU	P04575 mesocricetu	680	203	8.4	322	2	09D6D0	09D6D0 mus muscu
608	213	8.8	313	1	M2OM_HUMAN	002978 homo sapien	681	203	8.4	286	2	09FX05	09FX05 triticum ae
609	213	8.8	318	2	08INK4	08INK4 drosophila	682	203	8.4	304	2	065YS1	065YS1 dracunculus
610	212.5	8.8	297	2	06CRN3	06CRN3 kluyveromyc	683	203	8.4	361	2	08NCF7	08NCF7 homo sapien
611	212.5	8.8	319	2	08IND3	08IND3 drosophila	684	201.5	8.3	287	1	DIC_HUMAN	09UBX3 homo sapien
612	212.5	8.8	326	2	091XD8	091XD8 m cdna sequ	685	201.5	8.3	306	1	UCPI_MOUSE	P12242 mus musculu
613	212	8.7	274	2	06CS09	06CS09 kluyveromyc	686	201.5	8.3	347	2	09NYZ2	09NYZ2 homo sapien
614	212	8.7	299	1	ODC_HUMAN	09BQ68 homo sapien	687	201	8.3	292	1	ORT1 YEAST	012375 saccharomyc
615	212	8.7	299	2	09VMS1	09VMS1 drosophila	688	201	8.3	307	2	08K404	08K404 dicostomyc

689	201	8.3	360	2	Q76NQ2	Q76nq2	drosophila	762	190	7.8	305	2	Q6C5J8	Q6C5j8	yarrowia 11
690	201	8.3	332	2	Q8IH44	Q8ih44	drosophila	763	190	7.8	316	2	Q6CA10	Q6ca10	yarrowia 11
691	201	8.3	399	2	Q9VKZ5	Q9vkz5	xenopus lae	764	190	7.8	332	2	Q8AVD9	Q8avd9	xenopus lae
692	200.5	8.3	291	2	O13844	O13844	schizosacch	765	190	7.8	338	2	Q7TPA1	Q7tpa1	rattus norv
693	200.5	8.3	377	2	Q6CMP2	Q6cmp2	kluyveromyc	766	190	7.8	344	2	Q7PZU7	Q7pzu7	anopheles g
694	200	8.3	304	2	Q8LWZ1	Q8lwnz1	helicodicer	767	189.5	7.8	275	2	Q6RSJ6	Q6rsj6	rattus norv
695	200	8.3	306	2	Q8SA58	Q8sa58	lycoperisico	768	189.5	7.8	366	2	Q8O413	Q8o413	zea mays 1m
696	200	8.3	333	2	Q8LKU9	Q8lku9	sorghum bic	769	189.5	7.8	414	2	Q6ZA15	Q6za15	oryza sativ
697	200	8.3	340	2	Q8WZM4	Q8wzm4	neurospora	770	189	7.8	300	2	Q6BRJ6	Q6brj6	paramecium
698	199.5	8.2	238	2	Q6SA73	Q6sa73	cyrtinus ca	771	188.5	7.8	232	2	Q6C0B0	Q6c0b0	yarrowia 11
699	199.5	8.2	286	2	Q6NRR4	Q6nrr4	xenopus lae	772	188.5	7.8	297	2	Q7PDE9	Q7pde9	anopheles g
700	199.5	8.2	311	1	TXTP_HUMAN	TXtp_HUMAN	homo sapien	773	188.5	7.8	323	2	Q949U9	Q949u9	anopheles g
701	199.5	8.2	318	2	Q6LAP8	Q6lap8	homo sapien	774	188	7.8	224	2	Q6Y120	Q6y120	eremotheciu
702	199.5	8.2	360	2	Q6P7N3	Q6p7n3	xenopus tiro	775	188	7.8	287	2	Q8T406	Q8t406	drosophila
703	199	8.2	284	1	PET8_YEAST	P89n21	saccharomyc	776	188	7.8	293	2	Q9V349	Q9v349	drosophila
704	199	8.2	306	2	O243J1	O243j1	solanum tub	777	188	7.8	299	1	TXTP_YEAST	P38152	saccharomyc
705	199	8.2	431	2	Q7S8I9	Q7s8i9	neurospora	778	188	7.8	302	2	Q6BI45	Q6bi45	debaromyce
706	199	8.2	441	2	Q8IQM4	Q8iqm4	drosophila	779	188	7.8	302	2	Q7Q9H1	Q7q9h1	anopheles g
707	198.5	8.2	285	2	Q21800	Q21800	caenorhabdl	780	188	7.8	321	2	Q9FNU5	Q9fnu5	oryza sativ
708	198.5	8.2	330	2	Q8RU49	Q8ru49	oryza sativ	781	188	7.8	332	2	Q6P1T7	Q6p1t7	xenopus tiro
709	198	8.2	246	2	Q8N413	Q8n413	homo sapien	782	188	7.8	336	2	Q81487	Q81487	arabidopsis
710	198	8.2	288	1	UCPL_BOVIN	P10861	bos taurus	783	188	7.8	342	2	Q93VZ9	Q93vz9	arabidopsis
711	198	8.2	301	2	Q6FW74	Q6fwt4	candida gla	784	187.5	7.7	209	2	Q7T3C5	Q7t3c5	ratu
712	197.5	8.2	210	2	Q8R206	Q8r206	mus muscicu	785	187.5	7.7	334	2	Q86ZJ2	Q86zj2	podospora a
713	197.5	8.2	218	2	Q9ZP17	Q9zpt7	gracillaria	786	187	7.7	345	1	IDES_SCHPO	Q10432	schizosacch
714	197.5	8.2	337	2	Q9FY68	Q9fy68	arabidopsis	787	186.5	7.7	224	2	Q8Q696	Q8q696	pagrus majo
715	197	8.1	302	2	Q7QJ46	Q7qj46	anopheles g	788	186.5	7.7	339	2	Q9VC40	Q9vc40	drosophila
716	197	8.1	310	2	Q6GLH4	Q6glh4	xenopus tiro	789	186.5	7.7	360	2	Q7XV24	Q7xv24	oryza sativ
717	197	8.1	322	2	Q8SAE3	Q8sae3	triticum mo	790	186	7.7	305	2	Q6IMH3	Q6imh3	xenopus lae
718	197	8.1	348	2	Q96U08	Q96u08	neurospora	791	186	7.7	306	2	Q7QJ40	Q7qj40	anopheles g
719	196.5	8.1	327	1	CRC1_YEAST	Q12289	saccharomyc	792	186	7.7	315	2	Q6C780	Q6c780	yarrowia 11
720	196.5	8.1	335	2	Q9VMK1	Q9vmk1	drosophila	793	186	7.7	329	2	Q7SBA1	Q7sba1	ashhya goes
721	196.5	8.1	340	1	Q6BH02	Q6bh02	debaromyce	794	186	7.7	344	2	Q9EPH6	Q9eph6	rattus norv
722	196	8.1	298	1	ODC_RAT	Q99i33	rattus norv	795	185.5	7.7	286	2	Q89035	Q89035	rattus norv
723	196	8.1	303	2	Q6FBC0	Q6fbc0	candida gla	796	185.5	7.7	303	2	Q9VB24	Q9vb24	arabidopsis
724	196	8.1	303	2	Q9MBE7	Q9mbd7	symlocarpa	797	185.5	7.7	323	2	Q8ID58	Q8id58	arabidopsis
725	196	8.1	304	2	Q9V6T0	Q9v6t0	drosophila	798	185	7.6	342	2	Q6BI42	Q6bi42	debaromyce
726	196	8.1	307	2	Q6BWD5	Q6bwd5	debaromyce	799	184.5	7.6	301	2	Q10050	Q10050	caenorhabdl
727	196	8.1	331	2	Q6DHS4	Q6dhs4	brachydantio	800	184.5	7.6	296	2	Q66PX7	Q66px7	saccharum o
728	195.5	8.1	265	2	Q99ML6	Q99ml6	mus muscicu	801	183.5	7.6	303	2	Q6CVY2	Q6cvy2	kluyveromyc
729	195.5	8.1	332	2	O18390	O18390	caenorhabdl	802	183.5	7.6	368	2	Q8O414	Q8o414	oryza sativ
730	195	8.0	326	2	Q9Y7G4	Q9y7g4	emeticella	803	183.5	7.6	375	2	Q8O412	Q8o412	glycine max
731	194.5	8.0	356	1	MPCP_RAT	P16036	rattus norv	804	183.5	7.6	413	2	Q944H5	Q944h5	arabidopsis
732	194.5	8.0	364	2	P93070	P93070	betula veir	805	183	7.6	337	2	Q9VVK0	Q9vmk0	arabidopsis
733	194	8.0	297	2	Q6FR88	Q6fr88	candida gla	806	182.5	7.5	252	2	Q9CRC7	Q9crc7	mus muscicu
734	194	8.0	342	2	Q8L9F8	Q8l9f8	arabidopsis	807	182.5	7.5	286	2	Q7ZWA7	Q7zwa7	brachydantio
735	194	8.0	369	2	Q6CI09	Q6ci09	arabidopsis	808	182.5	7.5	349	2	Q9SSP4	Q9ssp4	arabidopsis
736	194	8.0	374	2	Q9V916	Q9v916	yarrowia 11	809	182	7.5	194	2	Q8NR46	Q8nr46	homo sapien
737	193.5	8.0	284	2	Q6CPR6	Q6cpr6	drosophila	810	182	7.5	307	2	Q07534	Q07534	saccharomyc
738	193.5	8.0	296	2	Q6BLR3	Q6blr3	debaromyce	811	182	7.5	314	2	Q6CDB3	Q6cdb3	yarrowia 11
739	193.5	8.0	357	2	Q6IRH6	Q6irh6	rattus norv	812	182	7.5	334	2	Q7QBND6	Q7qbnd6	anopheles g
740	193.5	8.0	362	1	MPCP_BOVIN	P12234	bos taurus	813	181.5	7.5	177	2	Q8R578	Q8r578	mus muscicu
741	193	8.0	241	2	Q8WIA3	Q8wia3	glycine max	814	181.5	7.5	342	2	Q8W198	Q8w198	glycine max
742	193	8.0	322	2	Q9ARI9	Q9ari9	hordeum vul	815	181.5	7.5	369	2	Q8GZJ3	Q8gzj3	arabidopsis
743	192.5	7.9	293	2	Q6BT74	Q6bt74	debaromyce	816	181.5	7.5	1796	2	Q7S6P3	Q7s6p3	neurospora
744	192.5	7.9	306	2	Q9P5U2	Q9p5u2	neurospora	817	180.5	7.4	177	2	Q8K4J9	Q8k4j9	mus muscicu
745	192.5	7.9	335	2	Q69FA0	Q69fa0	phaseolus v	818	180.5	7.4	300	2	Q9VLF1	Q9vlf1	drosophila
746	192.5	7.9	342	2	Q7S952	Q7s952	neurospora	819	180.5	7.4	335	2	Q9PFX9	Q9pfx9	schizosacch
747	192.5	7.9	357	1	MPCP_MOUSE	Q8vem8	mus muscicu	820	180.5	7.4	356	2	Q8WVY1	Q8wvy1	lotus japon
748	192.5	7.9	365	2	Q9EPH5	Q9eph5	rattus norv	821	180	7.4	242	2	Q94FU6	Q94fu6	mangifera 1
749	192	7.9	284	2	Q6BX69	Q6bx69	debaromyce	822	180	7.4	310	1	ODCI_YEAST	Q03028	saccharomyc
750	191.5	7.9	289	2	Q62347	Q62347	caenorhabdl	823	180	7.4	338	2	Q6CTE0	Q6cte0	kluyveromyc
751	191.5	7.9	326	2	Q8X1Z8	Q8x1z8	americeella	824	180	7.4	344	2	Q7R7S6	Q7r7s6	plasmodium
752	191	7.9	282	2	Q6FSJ3	Q6fsj3	candida gla	825	180	7.4	436	2	Q86JN8	Q86jn8	dicyostel
753	191	7.9	307	2	Q9QYH1	Q9qyh1	mus muscicu	826	179.5	7.4	368	2	Q69FX3	Q69fx3	oryza sativ
754	191	7.9	313	1	M2OM_RAT	P97700	rattus norv	827	179	7.4	160	1	TPCS_ANGAN	P81660	anguilla an
755	190.5	7.9	296	2	Q9P6N6	Q9p6n6	schizosacch	828	179	7.4	160	2	Q918U8	Q918u8	brachydantio
756	190.5	7.9	303	2	Q48703	Q48703	arabidopsis	829	179	7.4	184	2	Q6PL49	Q6pl49	homo sapien
757	190.5	7.9	331	2	Q04200	Q04200	arabidopsis	830	179	7.4	280	2	Q6BIF3	Q6bif3	debaromyce
758	190.5	7.9	331	2	Q8L9P5	Q8l9p5	arabidopsis	831	179	7.4	295	2	Q7S6J8	Q7s6j8	neurospora
759	190.5	7.9	382	2	Q7SD41	Q7sd41	neurospora	832	178.5	7.4	263	2	Q7S0X6	Q7s0x6	neurospora
760	190.5	7.9	393	2	Q9XUK1	Q9xuk1	caenorhabdl	833	178.5	7.4	297	2	Q9VBN7	Q9vbn7	drosophila
761	190	7.8	156	2	Q67Z18	Q67z18	arabidopsis	834	178	7.3	289	2	Q6CGA0	Q6cga0	yarrowia 11

835	178	7.3	341	2	06B051	06bq51 debaryomyce	908	163.5	6.7	295	2	06FTN2	06ftn2 candida gla
836	177.5	7.3	311	2	09P7v8	09p7v8 schizosacch	909	163	6.7	172	2	08B214	08b214 mus musculu
837	177.5	7.3	319	2	Q7Y90	Q7y90 cryptospori	910	163	6.7	187	2	09P012	09p012 homo sapien
838	177.5	7.3	419	2	000324	000324 candida boi	911	163	6.7	350	2	06B016	06b016 debaryomyce
839	177	7.3	309	2	Q7PRX5	Q7prx5 anopheles g	912	162.5	6.7	161	2	076C81	076c81 tracheomye s
840	176.5	7.3	240	2	Q9VGF6	Q9vgf6 drosophila	913	162.5	6.7	162	1	TPCS_MELGA	P10246 melaeagris s
841	176.5	7.3	268	2	Q9MBE6	Q9mbe6 symlocarpu	914	162.5	6.7	228	2	070KX8	07qkx8 anopheles g
842	176.5	7.3	303	2	Q9V6X9	Q9v6x9 drosophila	915	162.5	6.7	309	2	06D8H9	06d8h9 brachydantio
843	176	7.3	363	2	Q9M2Z8	Q9m2z8 arabidopsis	916	162.5	6.7	323	2	061S41	061s41 mus musculu
844	175.5	7.2	246	2	Q66K17	Q66k17 xenopus lae	917	162.5	6.7	324	2	07TPP3	07tpp3 mus musculu
845	175.5	7.2	280	2	Q9Y166	Q9y166 drosophila	918	162	6.7	295	2	08SFO3	08sfo3 nicotiana t
846	175.5	7.2	373	2	Q19422	Q19422 caenorhabdi	919	162	6.7	300	1	PIC2_YEAST	P40035 saccharomyc
847	175	7.2	294	2	Q6CYN8	Q6cyn8 kluyveromyc	920	162	6.7	304	2	Q9VDM3	Q9vdm3 drosophila
848	175	7.2	304	2	Q7RMK9	Q7rmk9 neurospora	921	162	6.7	307	2	Q6CNU2	Q6cnu2 kluyveromyc
849	175	7.2	309	2	Q7SB09	Q7sb09 neurospora	922	162	6.7	336	2	Q6BMR7	Q6bmr7 debaryomyce
850	175	7.2	344	2	Q84Q49	Q84q49 oryza sativ	923	161.5	6.7	161	2	Q8AUR4	Q8aur4 xenopus lae
851	175	7.2	351	2	Q84X74	Q84x74 chlamydomon	924	161.5	6.7	163	2	Q12997	Q12997 xenopus lae
852	174.5	7.2	340	2	Q7SA82	Q7sa82 aahbya goss	925	161.5	6.7	298	2	Q9CSM0	Q9csm0 arabidopsis
853	174.5	7.2	353	2	Q9LFW2	Q9lfw2 arabidopsis	926	161.5	6.7	337	2	Q6CCV8	Q6ccv8 yarrowia li
854	174.5	7.2	503	2	Q9NEA3	Q9nea3 leishmania	927	161	6.6	287	2	Q707Y9	Q707y9 dichia angu
855	174	7.2	319	2	Q6CVD7	Q6cvd7 kluyveromyc	928	160.5	6.6	162	1	TPCS_RANES	P02589 rana esculie
856	173.5	7.2	365	2	Q86Z12	Q86z12 neurospora	929	160.5	6.6	302	2	Q40918	Q40918 panicum mil
857	173	7.1	300	2	Q6BK67	Q6bk67 debaryomyce	930	160	6.6	283	2	Q9CX10	Q9cx10 mus musculu
858	173	7.1	419	1	P47B_CANBO	Q00319 candida boi	931	159.5	6.6	161	2	Q6P8B2	Q6p8b2 xenopus tro
859	172.5	7.1	207	2	Q86CZ8	Q86cz8 caenorhabdi	932	159.5	6.6	163	2	Q12996	Q12996 xenopus lae
860	172	7.1	245	2	Q8N518	Q8n518 homo sapien	933	159.5	6.6	176	2	Q9H2J3	Q9h2j3 homo sapien
861	171.5	7.1	170	2	Q9X859	Q9x859 sus scrota	934	159.5	6.6	307	2	Q66PW8	Q66pw8 saccharum o
862	171.5	7.1	307	2	Q6CJX8	Q6cjx8 kluyveromyc	935	159	6.6	160	2	Q76C79	Q76c79 alligator m
863	171.5	7.1	423	1	P47A_CANBO	P12245 candida boi	936	159	6.6	301	2	Q9Y7D8	Q9y7d8 aspergillus
864	171.5	7.1	183	2	P905F8	P905f8 oxytricha t	937	159	6.6	329	1	YMC2_YEAST	P38087 saccharomyc
865	171	7.1	241	2	Q8M1A4	Q8m1a4 glycine max	938	158.5	6.5	302	2	Q42432	Q42432 panicum mil
866	171	7.1	245	2	Q67U56	Q6u56 oryza sativ	939	158.5	6.5	385	2	Q92228	Q92228 emericella
867	171	7.1	309	2	Q75DP0	Q75dp0 aahbya goss	940	158	6.5	149	2	Q86M81	Q86m81 tetralymena
868	171	7.1	310	2	Q18844	Q18844 caenorhabdi	941	158	6.5	854	2	Q7XF20	Q7xf20 oryza sativ
869	171	7.1	324	1	QAC1_YEAST	P32332 saccharomyc	942	158	6.5	854	2	Q9AYE7	Q9aye7 oryza sativ
870	171	7.1	360	2	Q814M0	Q814m0 caenorhabdi	943	157.5	6.5	201	2	P92028	P92028 drosophila
871	170.5	7.0	177	2	Q969G8	Q969g8 homo sapien	944	157.5	6.5	297	2	Q43649	Q43649 solanum tub
872	170.5	7.0	298	2	Q06143	Q06143 saccharomyc	945	157	6.5	320	2	Q6FM23	Q6fm23 candida gla
873	170.5	7.0	307	1	YMC1_YEAST	P22331 saccharomyc	946	156.5	6.5	150	1	TPCA_HOMAM	P29230 homartus ame
874	170.5	7.0	319	2	Q6PH61	Q6ph61 brachydanio	947	156.5	6.5	162	1	TPCS_CHICK	P02588 gallus galli
875	170.5	7.0	344	2	Q753S3	Q753s3 aahbya goss	948	156.5	6.5	318	2	Q81B13	Q81b13 plasmodium
876	170.5	7.0	375	2	Q9FMU6	Q9fmu6 arabidopsis	949	156	6.4	306	2	Q6BHR7	Q6bhr7 debaryomyce
877	170	7.0	295	2	Q8J209	Q8j209 gibberella	950	155.5	6.4	159	1	TPCS_MOUSE	P20801 mus musculu
878	170	7.0	299	2	Q6T871	Q6t871 citrus junu	951	155.5	6.4	317	2	Q6C737	Q6c737 yarrowia li
879	170	7.0	311	2	Q6FLZ8	Q6flz8 candida gla	952	155.5	6.4	319	2	Q7RMU4	Q7rmu4 plasmodium
880	170	7.0	324	2	Q871V0	Q871v0 neurospora	953	155.5	6.4	335	2	Q81QM3	Q81qm3 drosophila
881	170	7.0	335	2	Q6BTB9	Q6btb9 debaryomyce	954	155	6.4	155	2	Q6XJ25	Q6xj25 drosophila
882	170	7.0	349	1	MPCP_CHOFU	Q61703 choriastoneu	955	155	6.4	155	2	Q9V5V9	Q9v5v9 mus musculu
883	170	7.0	357	2	Q67UJ2	Q67uaj2 oryza sativ	956	155	6.4	187	2	Q9CG67	Q9cg67 m mus muscu
884	169.5	7.0	287	1	DIC_MOUSE	Q9qzde mus musculu	957	155	6.4	312	2	Q7YVD5	Q7yvd5 trypanosoma
885	169.5	7.0	288	2	Q80415	Q80415 arabidopsis	958	154.5	6.4	159	1	TPCS_PIG	P02587 sus scrota
886	169.5	7.0	307	2	Q8MLB9	Q8mlb9 drosophila	959	154.5	6.4	305	2	Q9UVG0	Q9uvy0 tuber magna
887	169.5	7.0	336	2	Q6CCX5	Q6ccx5 yarrowia li	960	154	6.4	160	2	Q76C80	Q76c80 sceloporuss
888	169	7.0	250	2	Q65YR9	Q65yr9 yarrowia li	961	154	6.4	186	2	Q96E88	Q96e88 homo sapien
889	169	7.0	322	2	Q6FVX5	Q6fvy5 philodendro	962	154	6.4	258	2	Q94344	Q94344 schizosacch
890	168.5	7.0	271	1	YADB_SCHPO	Q09834 candida gla	963	153.5	6.3	328	2	Q86U14	Q86u14 homo sapien
891	168.5	7.0	297	2	Q6FLN4	Q6fln4 schizosacch	964	153	6.3	338	2	Q7W510	Q7w510 fusarium ox
892	168.5	7.0	329	2	Q6FWY1	Q6fwy1 candida gla	965	153	6.3	152	2	Q6C3K3	Q6c3k3 yarrowia li
893	168	6.9	304	2	Q6CPR7	Q6cpr7 kluyveromyc	966	153	6.3	304	2	Q6PIV7	Q6piv7 homo sapien
894	167.5	6.9	305	2	Q6FWA9	Q6fwa9 candida gla	967	152.5	6.3	159	1	TPCS_RABIT	P02586 oryctolagus
895	167.5	6.9	310	2	Q6J3Z9	Q6j3z9 retusus norv	968	152.5	6.3	160	2	Q6PVW3	Q6pvw3 sus scrota
896	167	6.9	193	2	Q9N1D8	Q9nid8 macaca mula	969	152.5	6.3	161	2	Q61O64	Q61o64 brachydantio
897	167	6.9	300	2	Q8SFO2	Q8sfo2 nicotiana t	970	152	6.3	335	2	Q96U23	Q96u23 neurospora
898	166.5	6.9	317	2	Q6FXM7	Q6fxm7 candida gla	971	152	6.3	340	2	Q81YV9	Q81yv9 plasmodium
899	166	6.9	297	2	Q9FSP4	Q9fsp4 drosophila	972	151	6.2	144	2	Q876C1	Q876c1 saccharomyc
900	166	6.9	343	2	Q9FSP4	Q9fsf4 nicotiana t	973	151	6.2	155	2	Q81G72	Q81g72 drosophila
901	166	6.9	301	2	Q6CYE7	Q6cye7 kluyveromyc	974	151	6.2	213	2	Q9SMK6	Q9smk6 cicer ariet
902	166	6.8	297	2	Q8SP04	Q8sp04 nicotiana t	975	150.5	6.2	308	2	Q6Q0C1	Q6q0c1 homo sapien
903	165	6.8	360	2	Q6CJN8	Q6cjn8 yarrowia li	976	149.5	6.2	155	2	Q9N1B0	Q9nie0 macaca mula
904	164.5	6.8	129	2	Q6PN71	Q6pn71 aptenodyces	977	149.5	6.2	158	2	Q6XJ19	Q6xj19 drosophila
905	164.5	6.8	292	2	Q9LG45	Q9lg45 oryza sativ	978	149.5	6.2	320	2	Q9UTN1	Q9utn1 schizosacch
906	164.5	6.8	358	2	Q8S8M6	Q8s8m6 arabidopsis	979	149	6.1	447	2	Q7S114	Q7s114 neurospora
907	164	6.8	344	2	P93016	P93016 arabidopsis	980	148	6.1	148	1	CALM_AJBICA	Pe0206 ajellowyces

981	148	6.1	148	1	CALM_ASPOR	Pe0205 aspergillus	1054	140.5	5.8	243	1	LPSE_LYPI	003975 lytechinus
982	148	6.1	148	1	CALM_COGL	Pe1861 collictric	1055	140.5	5.8	282	2	Q6CBY2	06cb2 yarrowia li
983	148	6.1	148	1	CALM_COGL	Pe1860 collictric	1056	140.5	5.8	149	2	Q6DBP8	09dbp8 mus musculu
984	148	6.1	148	1	CALM_EMENTI	Pe0204 emericella	1057	140	5.8	151	1	CALM_PNECA	P41041 pneumocysti
985	148	6.1	148	1	CALM_NEUCR	Pe1859 neurospora	1058	140	5.8	161	1	TPCC_BOVIN	Pe3315 bos taurus
986	148	6.1	149	2	Q71KE2	Q71ke2 paracoccidi	1059	140	5.8	161	1	TPCC_CHICK	P09860 gallus gall
987	148	6.1	151	2	Q6WEX0	Q6wex0 dirosophila	1060	140	5.8	161	1	TPCC_PTC	P63317 sus scrofa
988	148	6.1	155	1	TPC2_DROME	Pa7948 dirosophila	1061	140	5.8	161	2	Q7ZDB9	07zdb9 oncorhynch
989	148	6.1	306	2	Q6FXQ6	Q6fxq6 candida gla	1062	139.5	5.8	121	2	Q6Y1S3	06y1s3 bos taurus
990	148	6.1	328	2	Q06497	Q06497 saccharomyc	1063	139.5	5.7	148	2	Q6BS94	06bs94 debaryomyc
991	148	6.1	378	2	Q84O91	Q84q91 cryza sattiv	1064	139	5.7	150	2	Q39890	039890 glycine max
992	148	6.1	387	2	Q8STY0	Q8sty0 dirosophila	1065	139	5.7	152	2	Q7QCA9	07qca9 anopheles g
993	148	6.1	426	2	Q9NF73	Q9nf73 dirosophila	1066	139	5.7	230	2	Q9SCA1	09sca1 lotus japon
994	147.5	6.1	145	2	Q9BON9	Q9bqn9 homo sapien	1067	138.5	5.7	161	2	Q800V7	0800v7 brachydanio
995	147.5	6.1	159	2	TPCS_HUMAN	P02585 homo sapien	1068	138.5	5.7	306	2	Q8WB66	Q8wb66 m mus muscu
996	147.5	6.1	182	2	Q18058	Q18058 caenorhabdi	1069	138.5	5.7	368	2	Q6C1K1	06c1k1 yarrowia li
997	147	6.1	101	2	Q14553	Q14553 homo sapien	1070	138	5.7	161	1	TPCC_HUMAN	Pe3316 homo sapien
998	146	6.0	155	2	Q6IMT3	Q6imt3 dirosophila	1071	138	5.7	161	1	TPCC_RABIT	P02591 oryctolagus
999	146	6.0	162	1	CALM_CHURE	Pa4352 chlamydomon	1072	137.5	5.7	290	2	Q99RM5	099rm5 mus musculu
1000	146	6.0	164	2	P90687	P90687 brachiohisto	1073	137.5	5.7	300	2	Q9D913	09d913 m mus muscu
1001	146	6.0	164	2	P92198	P92198 dirosophila	1074	137	5.7	148	1	CALM_PATSP	P02595 patinopecte
1002	146	6.0	199	2	Q9V6Y1	Q9v6y1 dirosophila	1075	137	5.7	148	1	CALM_RENRE	Pe2184 renilla ren
1003	145.5	6.0	170	2	Q6RH07	Q6rh07 ciona intes	1076	137	5.7	148	1	CALM_SOLUT	P13868 solanum tub
1004	145.5	6.0	295	2	Q8N7F5	Q8n7f5 homo sapien	1077	137	5.7	166	2	Q9FYK2	09fyk2 arabisdopsis
1005	145.5	6.0	300	2	YHML_YEARST	P38968 saccharomyc	1078	136.5	5.6	161	2	Q12998	Q12998 xenopus lae
1006	145	6.0	122	2	Q70G13	Q70g13 aspergillus	1079	136.5	5.6	161	2	Q6DK95	06dk95 xenopus tiro
1007	145	6.0	122	2	Q70G14	Q70g14 aspergillus	1080	136.5	5.6	210	2	Q6RZU7	06rz07 musa acumin
1008	145	6.0	125	2	Q42267	Q42267 arabisdopsis	1081	136	5.6	147	2	Q6WEM8	Q6wem8 dirosophila
1009	145	6.0	126	2	Q7RVV3	Q7rvv3 neurospora	1082	136	5.6	148	1	CALM_BLAEM	Q9hf66 blastoccladi
1010	145	6.0	135	2	Q96TV0	Q96tv0 fusarium pr	1083	136	5.6	148	1	CALM_WHEAT	P04464 triticum ae
1011	145	6.0	148	1	CALM_MAGGR	Q9uwt0 magnaporthe	1084	136	5.6	149	2	Q99K52	099k52 mus musculu
1012	145	6.0	213	2	Q800V5	Q800v5 tetraodon f	1085	136	5.6	150	2	Q43447	Q43447 glycine max
1013	145	6.0	213	2	Q84P63	Q84p63 cryza sattiv	1086	136	5.6	169	1	CATR_CHURE	P05434 chlamydomon
1014	145	6.0	322	2	Q8LP98	Q8lp98 arabisdopsis	1087	136	5.6	173	2	Q9LJK5	09ljk5 arabisdopsis
1015	145	6.0	322	2	Q9MA90	Q9ma90 arabisdopsis	1088	135	5.6	399	2	Q9U0V1	Q9u0v1 leishmania
1016	145	6.0	591	2	Q39485	Q39485 chlamydomon	1089	135	5.6	148	1	CAL2_PETRY	P27163 petunia hyb
1017	144.5	6.0	110	2	Q8U0M1	Q8u0m1 yarrowia li	1090	135	5.6	148	2	Q6R2U7	Q6r2u7 acetunia hyp
1018	144.5	6.0	150	1	TPC1_HOMAM	P29289 homarus ame	1091	135	5.6	149	2	Q8LRJ0	Q8lrj0 ceratoplectr
1019	144.5	6.0	287	2	Q6RG63	Q6rg63 homo sapien	1092	135	5.6	149	2	Q9SDJ0	09sdj0 cryza sattiv
1020	144	5.9	150	2	Q94IG4	Q94ig4 nicotiana t	1093	135	5.6	363	1	AR13_NEUCR	Q9t131 canis famli
1021	144	5.9	150	2	Q40982	Q40982 pisum sattiv	1094	134.5	5.6	141	2	Q9TTT1	Q9ttt1 canis famli
1022	144	5.9	159	2	Q9SR67	Q9sr67 arabisdopsis	1095	134.5	5.6	149	2	Q711J0	Q711j0 solanum com
1023	144	5.9	162	2	Q26130	Q26130 plasmodium	1096	134.5	5.6	149	2	Q712P2	Q712p2 capsitum an
1024	144	5.9	164	2	Q75N06	Q75n06 brachiohisto	1097	134.5	5.6	149	2	Q76MF4	Q76mf4 nicotiana t
1025	143.5	5.9	148	1	CLM4_MOUSE	Q9jme3 mus musculu	1098	134.5	5.6	162	2	Q42137	Q42137 lampetra ja
1026	143.5	5.9	150	1	TPCB_HOMAM	P49291 homarus ame	1099	134.5	5.6	300	2	Q6FMQ9	Q6fmq9 candida gla
1027	143.5	5.9	167	2	Q42136	Q42136 lampetra ja	1100	134.5	5.6	550	2	Q9LDV2	Q9ldv2 arabisdopsis
1028	143	5.9	163	1	TPC1_BRALA	Pe0332 brachiohisto	1101	134	5.5	144	2	P90620	P90620 trichomonas
1029	143	5.9	299	2	Q7QKE0	Q7qke0 anopheles g	1102	134	5.5	148	1	CAL1_ARATH	P25854 arabisdopsis
1030	143	5.9	321	2	Q8VZ60	Q8vz60 arabisdopsis	1103	134	5.5	148	1	CAL2_ARATH	P25069 arabisdopsis
1031	143	5.9	377	2	Q7XK18	Q7xk18 cryza sattiv	1104	134	5.5	148	1	CAL6_ARATH	Q03509 arabisdopsis
1032	142.5	5.9	148	2	Q6WEM7	Q6wem7 mus musculu	1105	134	5.5	148	1	CALM_LYCES	P27161 lycopersico
1033	142.5	5.9	150	2	Q86M82	Q86m82 euploetes sp	1106	134	5.5	148	1	CALM_PHYPO	Q96102 phyarum po
1034	142.5	5.9	171	2	Q6IME1	Q6ime1 anopheles g	1107	134	5.5	148	2	Q7M215	Q7m215 pisum sattiv
1035	142.5	5.9	285	1	YFL5_YEARST	Pa3617 saccharomyc	1108	134	5.5	148	2	Q9LDQ9	Q9ldq9 chara coral
1036	142	5.9	147	1	TPC1_TODPA	Q9b1g0 todarodes p	1109	134	5.5	149	1	CALM_CANAL	P23286 candida alb
1037	142	5.9	151	2	Q6MEW7	Q6mew7 dirosophila	1110	134	5.5	149	2	Q6LDD3	Q6ldd3 brassica na
1038	142	5.9	151	2	Q23320	Q23320 arabisdopsis	1111	134	5.5	149	2	Q6LDD3	Q6ldd3 brassica ju
1039	142	5.9	155	1	TPC3_DROME	Pa7949 dirosophila	1112	134	5.5	152	2	Q9GN70	Q9gn70 perlinereis
1040	142	5.9	165	2	Q6IMT2	Q6imt2 dirosophila	1113	134	5.5	152	2	Q9SU00	Q9su00 arabisdopsis
1041	142	5.9	161	2	Q800V6	Q800v6 polypeterns	1114	134	5.5	258	2	Q74ZK9	Q74zk9 ashbya goss
1042	142	5.9	164	2	Q39708	Q39708 dunaliella	1115	133.5	5.5	153	2	Q6WEM9	Q6wem9 dirosophila
1043	142	5.9	186	2	Q7PP99	Q7pp99 anopheles g	1116	133.5	5.5	153	2	TPC1_BALNU	P21797 balanus nub
1044	142	5.9	341	2	Q9XTH0	Q9xth0 caenorhabdi	1117	133.5	5.5	160	1	TPC2_CABEL	Q09665 caenorhabdi
1045	141.5	5.8	150	1	TPC1_PONLE	Pe6707 pontastacus	1118	133.5	5.5	178	1	CALC_MOUSE	Pe3811 mus musculu
1046	141.5	5.8	175	1	CALC_RAT	P28470 rattus norv	1119	133.5	5.5	291	2	Q6ZT89	Q6zt89 homo sapien
1047	141.5	5.8	273	2	Q6Z8B0	Q6z8b0 cryza sattiv	1120	133.5	5.5	378	2	Q9SU04	Q9su04 arabisdopsis
1048	141.5	5.8	319	2	Q6C0X5	Q6c0x5 yarrowia li	1121	133	5.5	136	2	Q980B8	Q98ub8 clemmys jap
1049	141	5.8	148	1	Q9ATG1	Q9atg1 castanea sa	1122	133	5.5	145	2	Q09980	Q09980 caenorhabdi
1050	141	5.8	161	1	TPCC_MOUSE	P19123 mus musculu	1123	133	5.5	145	2	Q6IME6	Q6ime6 apis mellif
1051	141	5.8	169	1	Q7F0T0	Q7f0t0 cryza sattiv	1124	133	5.5	149	2	Q43412	Q43412 bidens pilo
1052	140.5	5.8	150	1	TPC2_PONLE	Pe6708 pontastacus	1125	133	5.5	151	2	Q868D2	Q868d2 lethocerus
1053	140.5	5.8	154	2	Q9N1D9	Q9n1d9 macaca mula	1126	133	5.5	167	2	Q23184	Q23184 arabisdopsis

1127	133	5.5	169	2	082659	082659 arabidopsis	1200	130.5	5.4	168	2	081272	081272 plasmidium
1128	133	5.5	222	2	081PK1	081PK1 drosophila	1201	130.5	5.4	304	2	08MWZ8	08MWZ8 neurospora
1129	133	5.5	297	2	056674	056674 schizosacch	1202	130.5	5.4	450	2	08T905	08T905 drosophila
1130	132.5	5.5	136	2	08C115	08C115 mus musculus	1203	130	5.4	148	2	06R2U4	06R2U4 atrachis hyp
1131	132.5	5.5	153	2	08SYD4	08SYD4 drosophila	1204	130	5.4	149	2	022641	022641 zea mays (m
1132	132.5	5.5	282	2	06BVS5	06BVS5 brachydanio	1205	130	5.4	149	2	06DN26	06DN26 daucus caro
1133	132.5	5.5	321	1	LPSCA	P03485 lycopersicon	1206	130	5.4	149	2	09M6U0	09M6U0 brasica na
1134	132.5	5.5	560	2	09SCMO	09SCMO arabidopsis	1207	130	5.4	150	1	CALM_SCHPO	P05933 schizosacch
1135	132	5.4	108	2	094FM8	094FM8 capsicum an	1208	130	5.4	161	1	TPCC_CORJA	P05936 coturnix co
1136	132	5.4	124	2	07DMP0	07DMP0 solanum tub	1209	130	5.4	297	1	MRT1_HUMAN	09H19 homo sapien
1137	132	5.4	137	2	084MW8	084MW8 brasica ol	1210	130	5.4	300	2	06CKS3	06CKS3 kluyveromyc
1138	132	5.4	148	1	CALM_CAPAN	P93087 capsicum an	1211	130	5.4	316	2	09P691	09P691 neurospora
1139	132	5.4	148	1	CALM_PYUSD	P11121 pyuridae sp	1212	129.5	5.3	150	2	086M84	086M84 nyctotherus
1140	132	5.4	149	2	042478	042478 solanum com	1213	129.5	5.3	150	2	086M86	086M86 nyctotherus
1141	132	5.4	149	2	043699	043699 zea mays (m	1214	129.5	5.3	156	2	08A7S5	08A7S5 borhrops in
1142	132	5.4	149	2	06L4B4	06L4B4 solanum dem	1215	129.5	5.3	176	2	084SBS	084SBS oryza sativ
1143	132	5.4	149	2	0710C9	0710C9 brasica ol	1216	129.5	5.3	215	2	022845	022845 arabidopsis
1144	132	5.4	149	2	076ME6	076ME6 nicotiana t	1217	129.5	5.3	271	2	06NRT14	06NRT14 brachydanio
1145	132	5.4	149	2	07DMN9	07DMN9 solanum tub	1218	129.5	5.3	450	2	09VJA5	09VJA5 drosophila
1146	132	5.4	155	1	CALF_NAEGR	P53440 neegleria g	1219	129	5.3	131	1	CALM_CHICK	P05419 gallus gall
1147	132	5.4	167	2	08LCE6	08LCE6 arabidopsis	1220	129	5.3	148	1	CALM_HUMAN	P27482 homo sapien
1148	132	5.4	355	2	06CVK6	06CVK6 kluyveromyc	1221	129	5.3	148	1	CALM_SUDO	P27482 suberites d
1149	131.5	5.4	151	1	CALM_DICDI	P02599 dictyostell	1222	129	5.3	149	2	043698	043698 zea mays (m
1150	131.5	5.4	158	2	086BD3	086BD3 lechoceus	1223	129	5.3	130	2	06CPT3	06CPT3 kluyveromyc
1151	131.5	5.4	248	2	07PGK6	07PGK6 anopheles g	1224	128.5	5.3	103	2	06CS35	06CS35 kluyveromyc
1152	131	5.4	118	2	070MW0	070MW0 fusarium pr	1225	128.5	5.3	150	2	086MB3	086MB3 nyctotherus
1153	131	5.4	122	2	082773	082773 nicotiana p	1226	128.5	5.3	153	1	TPC_TACTR	P15159 tachypneus
1154	131	5.4	135	2	09M428	09M428 oryza sativ	1227	128.5	5.3	172	2	093YF8	093YF8 sesbania ro
1155	131	5.4	142	1	P93603	P93603 triticum ae	1228	128.5	5.3	481	2	018652	018652 parametium
1156	131	5.4	148	1	CAL1_DAUCA	P62200 daucus caro	1229	128.5	5.3	595	2	09SDM4	09SDM4 dunaliella
1157	131	5.4	148	1	CAL1_PETRY	P62199 petunia hyb	1230	128	5.3	113	2	096HY3	096HY3 homo sapien
1158	131	5.4	148	1	CAL2_SOYBN	P62163 glycine max	1231	128	5.3	116	1	CALM_ORYLA	P62159 oryza sat
1159	131	5.4	148	1	CAL7_ARANT	P59220 arabidopsis	1232	128	5.3	136	2	091972	091972 oryza sat
1160	131	5.4	148	1	CALM_BRIDI	P62202 bryonia dio	1233	128	5.3	136	2	098SE9	098SE9 clemmys jap
1161	131	5.4	148	1	CALM_HELAN	P93171 helianthus	1234	128	5.3	141	1	CALA_ARAPU	P62146 arabicia pun
1162	131	5.4	148	1	CALM_HORVU	P62162 hordeum vul	1235	128	5.3	148	1	CALM_ANAPL	P62147 boas platyr
1163	131	5.4	148	1	CALM_LILLO	P62201 lillium long	1236	128	5.3	148	1	CALM_BOVIN	P62157 boas taurus
1164	131	5.4	148	1	CALM_MERDA	P17928 medicago sa	1237	128	5.3	148	1	CALM_BRARE	P62152 brachydanio
1165	131	5.4	148	1	CALM_ORYSA	P23612 oryza sativ	1238	128	5.3	148	1	CALM_CHICK	062152 gallus gall
1166	131	5.4	148	1	CALM_SPTOL	P04353 spinacia ol	1239	128	5.3	148	1	CALM_CIOIN	002357 cloas intes
1167	131	5.4	148	1	CAL5_CHICK	P02597 gallus gall	1240	128	5.3	148	1	CALM_EBEEL	P02594 electrophor
1168	131	5.4	148	1	08W0C0	08W0C0 stevia reba	1241	128	5.3	148	1	CALM_EPIAK	07C352 epinephelus
1169	131	5.4	149	2	049183	049183 oryza sativ	1242	128	5.3	148	1	CALM_HUMAN	P62158 homo sapien
1170	131	5.4	149	2	049184	049184 oryza sativ	1243	128	5.3	148	1	CALM_MOUSE	P62204 mus musculu
1171	131	5.4	149	2	P94058	P94058 triticum ae	1244	128	5.3	148	1	CALM_ONCSP	P62156 oncothychnu
1172	131	5.4	149	2	08L6D0	08L6D0 solanum com	1245	128	5.3	148	1	CALM_PAXIN	08X187 paxillus in
1173	131	5.4	149	2	093VL8	093VL8 phaseolus v	1246	128	5.3	148	1	CALM_RABIT	P62160 cryocolagus
1174	131	5.4	149	2	06DN29	06DN29 daucus caro	1247	128	5.3	148	1	CALM_RAT	P62161 rattus norv
1175	131	5.4	149	2	06DN31	06DN31 daucus caro	1248	128	5.3	148	1	CALM_STIJA	P62161 stichopus j
1176	131	5.4	149	2	06DN33	06DN33 daucus caro	1249	128	5.3	148	1	CALM_TORCA	P62151 torpedo cal
1177	131	5.4	149	2	06F332	06F332 oryza sativ	1250	128	5.3	148	1	CALM_TRYRB	P04465 trypanosoma
1178	131	5.4	149	2	06LBM2	06LBM2 malus domes	1251	128	5.3	148	1	CALM_TRYCR	P18061 trypanosoma
1179	131	5.4	149	2	06LVCY3	06LVCY3 pisum sativ	1252	128	5.3	148	1	CALM_XENTIA	P62155 xenopus lae
1180	131	5.4	149	2	06LBC4	06LBC4 vigna radia	1253	128	5.3	148	1	CALM_PLEOS	094739 pleuropus o
1181	131	5.4	149	2	06LBC8	06LBC8 glycine max	1254	128	5.3	148	2	06DMS1	06DMS1 salvia milt
1182	131	5.4	149	2	071JCS	071JCS medicago tr	1255	128	5.3	148	2	06R2U6	06R2U6 atrachis hyp
1183	131	5.4	149	2	071JCS	071JCS medicago tr	1256	128	5.3	149	2	066HK3	066HK3 homo sapien
1184	131	5.4	149	2	071SM1	071SM1 elaeis guin	1257	128	5.3	149	2	06VNX6	06VNX6 ovie aries
1185	131	5.4	149	2	071SM1	071SM1 prunus aviu	1258	128	5.3	149	2	039447	039447 capsicum an
1186	131	5.4	149	2	071V71	071V71 phaseolus v	1259	128	5.3	149	2	06DN35	06DN35 daucus caro
1187	131	5.4	149	2	071V71	071V71 phaseolus v	1260	128	5.3	149	2	09D6G4	09D6G4 mus musculu
1188	131	5.4	149	2	07DLR7	07DLR7 zea mays (m	1261	128	5.3	149	2	06DN21	06DN21 carassius a
1189	131	5.4	149	2	07DLR8	07DLR8 cicier ariet	1262	128	5.3	149	2	06IT78	06IT78 ctenopharyn
1190	131	5.4	149	2	07DMG9	07DMG9 triticum ae	1263	128	5.3	149	2	0710H6	0710H6 perca flav
1191	131	5.4	149	2	07DMG9	07DMG9 vigna radia	1264	128	5.3	149	2	0641U7	0641U7 xenopus tro
1192	131	5.4	149	2	07F8I8	07F8I8 oryza sativ	1265	128	5.3	177	2	09S014	09S014 nicotiana t
1193	131	5.4	149	2	07Y052	07Y052 euphorbia c	1266	127.5	5.3	149	2	07P8T7	07P8T7 anopheles g
1194	131	5.4	149	2	093410	093410 gallus gall	1267	127.5	5.3	156	2	018136	018136 caenorhabdi
1195	131	5.4	150	2	06UQ24	06UQ24 daucus caro	1268	127.5	5.3	161	2	07S2Z8	07S2Z8 xenopus lae
1196	131	5.4	154	1	SM20_SCHMA	P15845 schistosoma	1269	127.5	5.3	181	2	08TD86	08TD86 homo sapien
1197	131	5.4	154	1	086ET3	086ET3 echinotoma	1270	127.5	5.3	577	2	069IM9	069IM9 oryza sativ
1198	131	5.4	183	1	CAL3_PETRY	P27164 petunia hyb	1271	127	5.2	106	2	041981	041981 arabidopsis
1199	130.5	5.4	116	2	095XF6	095XF6 caenorhabdi	1272	127	5.2	132	2	08GVF3	08GVF3 arabidopsis

1273	127	5.2	138	1	CALB_ARBPU	P05932	arbacia pun	1346	123	5.1	148	1	CALM_STYLE	P27166	stylonychia
1274	127	5.2	146	2	Q6XH6	Q6xb6	drosophila	1347	123	5.1	149	2	Q7R9F4	Q7r9f4	plasmidium
1275	127	5.2	148	1	CAL1_BRAFL	Pe2148	branchiosto	1348	123	5.1	152	2	Q13942	Q13942	homo sapien
1276	127	5.2	148	1	CAL1_BRAFL	Pe2148	branchiosto	1349	123	5.1	177	2	Q9S0I5	Q9s0i5	nicotiana t
1277	127	5.2	148	1	CALB_HALRO	Pe2153	halocynthia	1350	123	5.1	225	2	Q45209	Q45209	branchiosto
1278	127	5.2	148	1	CALB_HALRO	Q96081	halocynthia	1351	123	5.1	359	2	Q9U0L1	Q9u0l1	plasmidium
1279	127	5.2	148	1	CALM_APICA	Pe2152	aplysia cal	1352	123	5.1	371	1	MNCP_OXYTR	Q27151	oxycricta t
1280	127	5.2	148	1	CALM_DROME	Pe2152	drosophila	1353	123	5.1	501	2	Q94094	Q94094	oryza sativ
1281	127	5.2	148	1	CALM_EUGRA	P1118	euglena gra	1354	123	5.1	530	2	Q93759	Q93759	arabidopsis
1282	127	5.2	148	1	CALM_HALOX	Q95n14	halichondri	1355	123	5.1	538	2	Q6NLO6	Q6nlo6	arabidopsis
1283	127	5.2	148	1	CALM_LOCOMI	Pe2154	locusta mig	1356	122.5	5.1	165	2	Q9W8U1	Q9w8u1	arabidopsis
1284	127	5.2	148	1	CALM_LOMRU	Q9gr11	lucidius r	1357	122	5.0	92	2	Q93XC1	Q93xc1	elaeis olei
1285	127	5.2	148	1	CALM_MERSE	Q95m9	metridius s	1358	122	5.0	140	2	Q25420	Q25420	leishmania
1286	127	5.2	148	1	CALM_PARTE	P07463	paramecium	1359	122	5.0	146	2	Q94801	Q94801	toxoplasma
1287	127	5.2	148	1	CALM_PLECO	P11103	pleurotus c	1360	122	5.0	148	1	CALM_PLAF7	Pe22033	plasmidium
1288	127	5.2	149	2	Q61305	O61305	caenorhabdi	1361	122	5.0	148	1	CALM_PLAFA	P24044	plasmidium
1289	127	5.2	149	2	Q66UB1	Q66ue1	culicoides	1362	122	5.0	148	1	CALM_TETPY	P02598	tetrahymena
1290	127	5.2	149	2	Q6BEV2	Q6eev2	pinctada fu	1363	122	5.0	149	2	Q8VYQ2	Q8vyq2	vitis vinif
1291	127	5.2	149	2	Q76LB7	Q76l7	strongyloce	1364	122	5.0	153	2	Q9SRR7	Q9srr7	arabidopsis
1292	127	5.2	149	2	Q92TV3	Q92tv3	phaseolus v	1365	122	5.0	154	2	Q84MNO	Q84mno	oryza sativ
1293	127	5.2	150	2	Q65347	O65347	apium grave	1366	122	5.0	161	2	Q6IMD8	Q6imd8	anopheles g
1294	127	5.2	155	1	CALM_STRIB	O8st6	strongyloce	1367	122	5.0	166	2	Q7PP00	Q7pp00	anopheles g
1295	127	5.2	176	2	Q7OC7	Q7gcy7	anopheles g	1368	122	5.0	166	2	Q948R0	Q948r0	oryza sativ
1296	126.5	5.2	153	2	Q6F437	Q6f437	pluteia xy	1369	122	5.0	223	2	Q6EMF2	Q6emf2	helianthus
1297	126	5.2	153	2	Q86C29	Q86c29	caenorhabdi	1370	122	5.0	259	2	Q6EPB8	Q6epb8	brachydanio
1298	126	5.2	129	2	Q9H0G8	Q9h0g8	homo sapien	1371	122	5.0	500	2	Q9U2J0	Q9u2j0	caenorhabdi
1299	126	5.2	148	1	CAL2_BRALA	Q9ub37	branchiosto	1372	122	5.0	583	2	Q7ROC8	Q7roc8	plasmidium
1300	126	5.2	148	1	CALM_MOUCS	O82018	mougeotia s	1373	121.5	5.0	115	2	Q99LQ9	Q99lq9	mus musculu
1301	126	5.2	148	1	CATR_SPESTI	P43665	spermatozop	1374	121.5	5.0	142	2	Q6IMH9	Q6imh9	drosophila
1302	126	5.2	167	1	CATR_ATRNU	P41210	atriplex nu	1375	121.5	5.0	147	1	CALM_FNGSX	Q39752	faqus sylva
1303	126	5.2	187	2	Q8S1Y9	Q8s1y9	oryza sativ	1376	121.5	5.0	169	1	CALB_BOVIN	Pe3099	bos taurus
1304	126	5.2	332	2	Q9VAB1	Q7s921	neurospora	1377	121.5	5.0	169	1	CALB_HUMAN	Pe3098	homo sapien
1305	126	5.2	332	2	Q9VAB1	Q9vab1	drosophila	1378	121.5	5.0	169	1	CALB_MOUSE	Q63810	mus musculu
1306	126	5.2	573	2	P93838	P93838	cucurbita p	1379	121.5	5.0	169	1	CALB_RAT	Pe3100	rattus norv
1307	126	5.2	1087	2	Q9UVN2	Q9uv72	drosophila	1380	121.5	5.0	170	2	Q66HZ0	Q66hz0	brachydanio
1308	125.5	5.2	154	2	Q9ZRO2	Q9zr02	arabidopsis	1381	121.5	5.0	170	2	Q6DUJ3	Q6duj3	xenopus lae
1309	125.5	5.2	154	2	Q867N3	Q867n3	paramecium	1382	121.5	5.0	170	2	Q6VNS0	Q6vns0	xenopus tro
1310	125	5.2	144	2	Q41420	Q41420	solanum tub	1383	121.5	5.0	170	2	Q6VNS1	Q6vns1	gallus gall
1311	125	5.2	134	2	O17501	O17501	branchiosto	1384	121.5	5.0	171	2	Q20804	Q20804	caenorhabdi
1312	125	5.2	148	1	CALM_MAIZE	P41040	zea mays (m	1385	121.5	5.0	221	2	O01256	O01256	caenorhabdi
1313	125	5.2	148	1	CALM_MAIZE	P41040	zea mays (m	1386	121.5	5.0	225	2	Q8M5C8	Q8m5c8	oryza sativ
1314	125	5.2	169	1	CATR_DUNSA	Pe4213	dunaliella	1387	121.5	5.0	225	2	Q75LJ8	Q75lj8	oryza sativ
1315	125	5.2	219	1	CAB2_HUMAN	Q9np3	homo sapien	1388	121.5	5.0	230	2	Q8LEM7	Q8lem7	arabidopsis
1316	125	5.2	226	2	Q8SF01	Q8sf01	nicotiana t	1389	121.5	5.0	534	2	Q6KCS3	Q6kcs3	nicotiana p
1317	124.5	5.1	140	2	Q7PIE1	Q7pie1	anopheles g	1390	121.5	5.0	765	2	Q86YX0	Q86yx0	homo sapien
1318	124.5	5.1	149	2	Q9BGR5	Q9bgr5	macaca fasc	1391	121	5.0	148	1	CALM_MALDO	Q96792	branchiosto
1319	124.5	5.1	150	2	Q86M85	Q86m85	nyctotherus	1392	121	5.0	151	2	Q96792	Q96792	branchiosto
1320	124.5	5.1	153	2	Q6IME0	Q6ime0	anopheles g	1393	121	5.0	153	2	Q27428	Q27428	chlamys nip
1321	124.5	5.1	153	2	Q6IME2	Q6ime2	aplis mellif	1394	121	5.0	168	1	CATR_SCHDU	Q0687	scherffelia
1322	124	5.1	97	2	Q91VO9	Q91vg9	mus musculu	1395	121	5.0	170	2	Q49939	Q49939	marisla ve
1323	124	5.1	147	2	Q9XZP3	Q9xzp3	branchiosto	1396	121	5.0	528	2	Q6F339	Q6f339	oryza sativ
1324	124	5.1	148	1	CALM_MXGL	Q9u6d3	myxine glut	1397	120.5	5.0	98	2	Q80K52	Q80k52	mus musculu
1325	124	5.1	148	1	CALM_PHYIN	P77165	phytophor	1398	120.5	5.0	121	2	Q8JHT7	Q8jht7	gadus morhu
1326	124	5.1	149	2	Q6W5T5	Q6w5t5	branchiosto	1399	120.5	5.0	153	2	Q8MRN4	Q8mrn4	solenopsis
1327	124	5.1	149	2	Q6DN30	Q6dn30	daucus caro	1400	120.5	5.0	161	2	P91328	P91328	caenorhabdi
1328	124	5.1	149	2	Q71UH5	Q71uh5	pythium spl	1401	120.5	5.0	271	2	Q8VHC5	Q8vhc5	mus musculu
1329	124	5.1	149	2	Q6RS20	Q6rs20	oreochromis	1402	120	5.0	107	2	Q9ATG2	Q9atg2	caecanea sa
1330	124	5.1	150	2	Q70560	Q70560	anopheles g	1403	120	5.0	148	1	CALB_DROME	P49258	drosophila
1331	124	5.1	155	2	Q8RLY3	Q8rly3	nostoc punc	1404	120	5.0	148	2	Q40303	Q40303	micromonas
1332	124	5.1	165	2	Q6PBP5	Q6pbp5	mus musculu	1405	120	5.0	153	2	Q95W98	Q95w98	giardia lam
1333	124	5.1	185	2	Q67T24	Q67t24	oryza sativ	1406	120	5.0	153	2	Q7QPK5	Q7qpk5	giardia lam
1334	123.5	5.1	150	2	Q39446	P15798	oxycricta f	1407	120	5.0	187	2	Q40642	Q40642	oryza sativ
1335	123.5	5.1	371	1	MNCP_OXYFA	Q39446	capricum an	1408	120	5.0	187	2	Q7G0S4	Q7g0s4	oryza sativ
1336	123.5	5.1	150	2	Q91NE7	Q91ne7	arabidopsis	1409	120	5.0	190	2	Q75CT2	Q75ct2	ashbya gos
1337	123.5	5.1	161	1	CALB_CAREL	P04630	caenorhabdi	1410	120	5.0	203	1	Q5CA2	BOVIN	bos taurus
1338	123.5	5.1	318	2	Q8TGD1	Q8tgd1	fusarium ox	1411	120	5.0	435	2	Q784K3	Q784k3	neurospora
1339	123.5	5.1	324	1	TCB3_ARATH	P25071	arabidopsis	1412	120	5.0	533	2	Q71S29	Q71s29	oryza sativ
1340	123.5	5.1	388	2	Q6BJY6	Q6bjy6	debrayomyce	1413	120	5.0	541	2	Q71S29	Q71s29	oryza sativ
1341	123.5	5.1	670	2	Q7RUZ4	Q7r14	plasmidium	1414	119.5	4.9	149	1	CABO_LOLPE	P14533	loligo peal
1342	123	5.1	133	2	Q6YND7	Q6ynd7	prococcenru	1415	119.5	4.9	149	2	C25383	Q25383	loligo peal
1343	123	5.1	138	2	O15931	O15931	symbiodininu	1416	119.5	4.9	154	1	TPC1_DROME	P47947	drosophila
1344	123	5.1	148	1	CAL2_BRAFL	Q9xzp2	branchiosto	1417	119.5	4.9	169	1	CALC_HUMAN	Q96123	homo sapien
1345	123	5.1	148	1	CALM_MACPY	Q40302	macrocyatis	1418	119.5	4.9	175	2	Q8LBR7	Q8lbr7	arabidopsis

1419	119.5	4.9	732	2	Q7R8Z9	Q7R8Z9 plasmodium
1420	119	4.9	133	2	Q40791	Q40791 pterospetma
1421	119	4.9	164	2	Q6L727	Q6L727 pterospetma
1422	119	4.9	173	1	CAB5_BOVIN	Q911q8 bos taurus
1423	118.5	4.9	149	2	Q8S460	Q8S460 sonneratia
1424	118.5	4.9	170	2	Q7T063	Q7T063 xenopus lae
1425	118.5	4.9	175	2	Q9LS47	Q9LS47 arabidopsis
1426	118.5	4.9	300	2	Q74439	Q74439 echinosach
1427	118	4.9	131	2	Q84NG2	Q84NG2 pyrus commu
1428	118	4.9	148	1	CATR_TEST	P35646 telisaelmis
1429	118	4.9	161	1	TCH2_ARATH	P25070 arabidopsis
1430	118	4.9	167	1	CET3_HUMAN	O15182 homo sapien
1431	117.5	4.8	182	2	Q7POV7	Q7POV7 anopheles g
1432	117.5	4.8	131	2	Q7PIE3	Q7PIE3 anopheles g
1433	117.5	4.8	225	2	Q8L7R6	Q8L7R6 plium sativ
1434	117.5	4.8	226	2	Q8L447	Q8L447 arabidopsis
1435	117	4.8	123	2	Q9GMX9	Q9GMX9 macaca fasc
1436	117	4.8	162	1	CAB2_BOVIN	Q911q9 bos taurus
1437	117	4.8	163	2	Q6L7Z6	Q6L7Z6 ochromonas
1438	117	4.8	167	2	Q6ICP7	Q6ICP7 homo sapien
1439	117	4.8	256	1	CSEN_RAT	Q91m4 ratulus norv
1440	117	4.8	279	2	Q8H2U4	Q8H2U4 bos taurus
1441	116.5	4.8	129	2	Q7PIE4	Q7PIE4 anopheles g
1442	116.5	4.8	164	2	Q6M4J2	Q6M4J2 ovis aries
1443	116.5	4.8	170	2	Q8N4Z2	Q8N4Z2 homo sapien
1444	116.5	4.8	186	2	Q7QJ14	Q7QJ14 anopheles g
1445	116.5	4.8	186	2	Q9W466	Q9W466 drosophila
1446	116.5	4.8	211	2	Q9AWK2	Q9AWK2 oryza sativ
1447	116.5	4.8	275	1	CAB4_HUMAN	P57796 homo sapien
1448	116.5	4.8	518	2	Q6KCK6	Q6KCK6 trititum ae
1449	116.5	4.8	527	1	CDP4_PLABA	P62345 plasmodium
1450	116.5	4.8	527	1	CDP4_PLAYO	Q7RJ92 cyprospori
1451	116.5	4.8	677	2	Q6S4W0	Q6S4W0 cyprospori
1452	116	4.8	89	2	Q17500	Q17500 brachiosteo
1453	116	4.8	140	2	Q6W3R0	Q6W3R0 mus musculu
1454	116	4.8	149	2	Q6DNZ5	Q6DNZ5 dancus caro
1455	116	4.8	152	1	TPC_PATYE	P35622 trititum ae
1456	116	4.8	157	2	Q8L6T8	Q8L6T8 arabidopsis
1457	116	4.8	157	2	Q9C8T1	Q9C8T1 arabidopsis
1458	116	4.8	198	2	Q8W4R8	Q8W4R8 homo sapien
1459	116	4.8	215	1	CAB2_MOUSE	Q9J1I4 mus musculu
1460	116	4.8	216	2	Q8JPF5	Q8JPF5 gallus gall
1461	116	4.8	226	2	Q9CSP6	Q9CSP6 arabidopsis
1462	116	4.8	226	2	Q9FVZ2	Q9FVZ2 arabidopsis
1463	116	4.8	236	1	CSEN_MOUSE	Q9QXK8 mus musculu
1464	116	4.8	256	2	Q924I0	Q924I0 mus musculu
1465	116	4.8	256	2	Q99P12	Q99P12 mus musculu
1466	116	4.8	284	2	Q99P10	Q99P10 mus musculu
1467	115.5	4.8	151	1	TPC2_BALNU	P21738 balanus nub
1468	115.5	4.8	167	2	Q6DH19	Q6DH19 brachydanio
1469	115.5	4.8	171	1	ALB8_OLEU	Q9M7X0 olea europae
1470	115.5	4.8	185	1	Q8RZB5	Q8RZB5 oryza sativ
1471	115.5	4.8	190	1	VISI_BOVIN	P62763 bos taurus
1472	115.5	4.8	190	1	VISI_CHICK	P62764 gallus gall
1473	115.5	4.8	190	1	VISI_HUMAN	P62760 homo sapien
1474	115.5	4.8	190	1	VISI_MOUSE	P62761 mus musculu
1475	115.5	4.8	190	1	VISI_RAT	P62762 ratulus norv
1476	115.5	4.8	190	1	VISI_RAT	P62762 ratulus norv
1477	115.5	4.8	256	2	Q6C501	Q6C501 yarrowia li
1478	115.5	4.8	256	2	Q8I513	Q8I513 plasmodium
1479	115.5	4.8	518	2	Q9AXA7	Q9AXA7 oryza sativ
1480	115.5	4.8	522	1	Q8H1T8	Q8H1T8 ceratopteri
1481	115.5	4.8	527	1	CDP4_PLAF7	Q8IB5 plasmodium
1482	115.5	4.8	527	1	Q6L5B7	Q6L5B7 oryza sativ
1483	115	4.7	980	2	Q9LOR4	Q9LOR4 arabidopsis
1484	115	4.7	159	2	Q91ZB8	Q91ZB8 ratulus norv
1485	115	4.7	167	1	CET3_MOUSE	Q35648 mus musculu
1486	115	4.7	167	1	Q9CVN1	Q9CVN1 mus musculu
1487	115	4.7	171	2	Q18092	Q18092 caenorhabdi
1488	115	4.7	173	1	CAB5_MOUSE	Q9J1K3 mus musculu
1489	115	4.7	187	2	Q9ZOB6	Q9ZOB6 arabidopsis
1490	115	4.7	187	2	Q6DTJ3	Q6DTJ3 mus musculu
1491	115	4.7	198	2	Q9BWT2	Q9BWT2 homo sapien
					Q6P8Y1	Q6P8Y1 mus musculu

1492	115	4.7	216	2	Q9H2A4	Q9H2A4 homo sapien
1493	115	4.7	216	2	Q9NMG8	Q9NMG8 ratulus norv
1494	115	4.7	229	2	Q8NEU0	Q8NEU0 homo sapien
1495	115	4.7	229	2	Q8R4I2	Q8R4I2 mus musculu
1496	115	4.7	229	2	Q8CAD0	Q8CAD0 mus musculu
1497	115	4.7	250	2	Q6PIL6	Q6PIL6 homo sapien
1498	115	4.7	250	2	Q9H294	Q9H294 homo sapien
1499	115	4.7	250	2	Q8HYN7	Q8HYN7 macaca fasc
1500	115	4.7	250	2	Q9NMG9	Q9NMG9 ratulus norv

ALIGNMENTS

RESULT 1						
Q6UX48	Q6UX48	PRELIMINARY;	PRT;	469 AA.		
AC	Q6UX48;					
DT	05-JUN-2004 (TREMBLrel. 27, Created)					
DT	05-JUN-2004 (TREMBLrel. 27, Last annotation update)					
DE	LCIC549.					
GN	ORENames=UNO549;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,					
RA	Chen J., Chow B., Chu C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Bacon D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Sehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagstad A.,					
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yamaura D.,					
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,					
RA	Godowski P.;					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment."					
RL	Genome Res. 13:2265-2270(2003).					
CC	-I- SIMILARITY: Belongs to the mitochondrial carrier family.					
DR	EMBL; AY358515; A088879.1; -.					
DR	HSSP; P09860; 1A74.					
DR	GO; GO:0016021; C:integral to membrane; IEA.					
DR	GO; GO:0005743; C:mitochondrial inner membrane; IEA.					
DR	GO; GO:0005488; F:binding; IEA.					
DR	GO; GO:0005509; F:calcium ion binding; IEA.					
DR	GO; GO:0005215; F:transporter activity; IEA.					
DR	InterPro; IPR002113; Aden translocator.					
DR	InterPro; IPR002048; EF-hand.					
DR	InterPro; IPR010983; EF-hand like.					
DR	InterPro; IPR002167; Graves_DC.					
DR	InterPro; IPR001993; Mitoch_carrier.					
DR	Pfam; PF00036; ehand; 3.					
DR	Pfam; PF00153; Mito_carr; 3.					
DR	PRINTS; PR00928; GRAVESDC.					
DR	PRINTS; PR00926; MITOCARRIER.					
DR	PRODOM; PD000012; EF-hand; 2.					
DR	SMART; SM00054; EFh; 3.					
DR	PROSITE; PS50920; SOLCAR; 3.					
KW	Transmembrane; Transport					
SQ	SEQUENCE 469 AA; 52689 MW; A0324982F613B5E CRC64;					
Query Match	100.0%;	Score 2423;	DB 2;	Length 469;		
Best Local Similarity	100.0%;	Pred. No. 1.7e-140;				
Matches 469;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		

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QY 1 MLCCLVVPVIGAGQTEFOYFESKGLPAELKSIIFKLSVFIPOSEFSTYRQMKIYVAGD 60
DB 1 MLCCLVVPVIGAGQTEFOYFESKGLPAELKSIIFKLSVFIPOSEFSTYRQMKIYVAGD 60
QY 61 KQIDGQDDEEFPHYLQDHEKRLVFKLIDKKNDGRIDAQEIQMSIRDLGVKISQOAE 120
DB 61 KQIDGQDDEEFPHYLQDHEKRLVFKLIDKKNDGRIDAQEIQMSIRDLGVKISQOAE 120
QY 121 KILKSMKDKGTMITDNNEMRDYHLHPVENIPEIILYMKHSTIFDVGENLTVPDEFTVEE 180
DB 121 KILKSMKDKGTMITDNNEMRDYHLHPVENIPEIILYMKHSTIFDVGENLTVPDEFTVEE 180
QY 181 RQCGMMWRHLVAGGAGAVSRCTAPLDRLKVLQMVHASSNNMGIVGGFTQMIREGGAR 240
DB 181 RQCGMMWRHLVAGGAGAVSRCTAPLDRLKVLQMVHASSNNMGIVGGFTQMIREGGAR 240
QY 241 SLWRGNGINVLKIAPESAIKFMAVEQIKRLVGSQDETLRIHERLVAGSLAGAIQSSIYP 300
DB 241 SLWRGNGINVLKIAPESAIKFMAVEQIKRLVGSQDETLRIHERLVAGSLAGAIQSSIYP 300
QY 301 MEVLKTRMALRKQYSGMLDCARRILAREGVAAFYKGYVPMNLGITIPYAGIDLAVYETL 360
DB 301 MEVLKTRMALRKQYSGMLDCARRILAREGVAAFYKGYVPMNLGITIPYAGIDLAVYETL 360
QY 361 KNAWLOHYAVNSADPGVFVLLACGTMSSTCGQLASYPALVTRMQOASIEGAPVYWS 420
DB 361 KNAWLOHYAVNSADPGVFVLLACGTMSSTCGQLASYPALVTRMQOASIEGAPVYWS 420
QY 421 SLFKHLIRTEGAGLYRGLAPNFMKVIPAVSISVYVENLKITLGVQSR 469
DB 421 SLFKHLIRTEGAGLYRGLAPNFMKVIPAVSISVYVENLKITLGVQSR 469

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RESULT 2

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ID 06KCM7 PRELIMINARY; PRT; 469 AA.
AC 06KCM7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Small calcium-binding mitochondrial carrier 2.
GN Name=SCAMC-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15054102; DOI=10.1074/jbc.M401417200;
RA del Arco A., Saturneque J.;
RT "Identification of a novel human subfamily of mitochondrial carriers
RT with calcium-binding domains.";
RL J. Biol. Chem. 279:24701-24713(2004).
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; AJ019989; CAF04495.1; -.
DR HSSP; P09860; 1AJ4.
DR GO; GO:0016021; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPRO02113; Aden translocor.
DR InterPro; IPRO02048; EF-hand.
DR InterPro; IPRO10983; EF-hand like.
DR InterPro; IPRO02167; Graves DC.
DR InterPro; IPRO01993; Mitoch carrier.
DR InterPro; IPRO02067; Mit carrier.
DR Pfam; PF00036; ehand; 3.
DR PRINTS; PRO0927; ADPTRSLCASE.
DR PRINTS; PRO0928; GRAVESDC.
DR PRINTS; PRO0926; MITOCARRIER.

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DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Eph; 3.
DR PROSITE; PS50920; SOLCAR; 3.
KW Transmembrane; Transport.
SQ SEQUENCE 469 AA; 52663 MW; A50825AA95DBD4BE CRC64;

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Query Match 99.8%; Score 2417; DB 2; Length 469;
Best Local Similarity 99.8%; Pred. No. 3.9e-140;
Matches 469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLCCLVVPVIGAGQTEFOYFESKGLPAELKSIIFKLSVFIPOSEFSTYRQMKIYVAGD 60
DB 1 MLCCLVVPVIGAGQTEFOYFESKGLPAELKSIIFKLSVFIPOSEFSTYRQMKIYVAGD 60
QY 61 KQIDGQDDEEFPHYLQDHEKRLVFKLIDKKNDGRIDAQEIQMSIRDLGVKISQOAE 120
DB 61 KQIDGQDDEEFPHYLQDHEKRLVFKLIDKKNDGRIDAQEIQMSIRDLGVKISQOAE 120
QY 121 KILKSMKDKGTMITDNNEMRDYHLHPVENIPEIILYMKHSTIFDVGENLTVPDEFTVEE 180
DB 121 KILKSMKDKGTMITDNNEMRDYHLHPVENIPEIILYMKHSTIFDVGENLTVPDEFTVEE 180
QY 181 RQCGMMWRHLVAGGAGAVSRCTAPLDRLKVLQMVHASSNNMGIVGGFTQMIREGGAR 240
DB 181 RQCGMMWRHLVAGGAGAVSRCTAPLDRLKVLQMVHASSNNMGIVGGFTQMIREGGAR 240
QY 241 SLWRGNGINVLKIAPESAIKFMAVEQIKRLVGSQDETLRIHERLVAGSLAGAIQSSIYP 300
DB 241 SLWRGNGINVLKIAPESAIKFMAVEQIKRLVGSQDETLRIHERLVAGSLAGAIQSSIYP 300
QY 301 MEVLKTRMALRKQYSGMLDCARRILAREGVAAFYKGYVPMNLGITIPYAGIDLAVYETL 360
DB 301 MEVLKTRMALRKQYSGMLDCARRILAREGVAAFYKGYVPMNLGITIPYAGIDLAVYETL 360
QY 361 KNAWLOHYAVNSADPGVFVLLACGTMSSTCGQLASYPALVTRMQOASIEGAPVYWS 420
DB 361 KNAWLOHYAVNSADPGVFVLLACGTMSSTCGQLASYPALVTRMQOASIEGAPVYWS 420
QY 421 SLFKHLIRTEGAGLYRGLAPNFMKVIPAVSISVYVENLKITLGVQSR 469
DB 421 SLFKHLIRTEGAGLYRGLAPNFMKVIPAVSISVYVENLKITLGVQSR 469

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RESULT 3

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ID 08K3P6 PRELIMINARY; PRT; 469 AA.
AC 08K3P6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Peroxisomal Ca-dependent solute carrier-like protein.
GN Name=Pscsl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22530605; PubMed=12645546; DOI=10.1074/jbc.M208398200;
RX Meshima H., Ueda N., Ohno H., Suzuki J., Ohnishi H., Yasuda H.,
RA Tsuchida T., Kanamaru C., Makita N., Iiri T., Onata M., Kojima I.;
RT "A novel mitochondrial Ca2+-dependent solute carrier in the liver
RT identified by mRNA differential display.";
RL J. Biol. Chem. 278:9520-9527(2003).
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; AY043169; AL05592.1; -.
DR HSSP; P02588; 1TNX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0006810; P:transport; IEA.

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DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_Like.
DR InterPro; IPR002167; Graves_DC.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mlt_carrier.
DR Pfam; PF00036; ehand; 3.
DR Pfam; PF00153; Mito_carr; 3.
DR PRINTS; PR00928; GRAVESDC.
DR PRINTS; PR00926; MITOCARRIER.
DR PRODOM; PD000012; EF-hand; 2.
DR PROSITE; PS50920; SOLCAR; 3.
DR Transmembrane; Transport.
KW SEQUENCE 469 AA; 52695 MW; 955SDA46B942992 CRC64;
Query Match 97.4%; Score 2360; DB 2; Length 469;
Best Local Similarity 96.8%; Pred. No. 1.2e-116;
Matches 454; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 MLCGLVVPVIGAEQTFQYFESKGLPAELKSIPLKLSVFIIPSOBFSTYRQWKQKIYQAGD 60
DB 1 MLCGLVVPVIGAEQTFQYFESKGLPAELKSIPLKLSVFIIPSOBFSTYRQWKQKIYQAGD 60
QY 61 KDLDGQDLFEFVHYLDHHEKRLVFKILDKKNDGRIDAQELMQSLRDLGVKISEQOAE 120
DB 61 KDLDGQDLFEFVHYLDHHEKRLVFKSLDKKNDGRIDAQELMQSLRDLGVKISEQOAE 120
QY 121 KILKMDKNGTMTIDNEMRDYHLHPVENIPETILYWKSTIPDVGBNLTPDEFTVEE 180
DB 121 KILKMDKNGTMTIDNEMRDYHLHPVENIPETILYWKSTIPDVGBNLTPDEFTVEE 180
QY 181 ROTGMMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNNNGIYGFQFMREGAK 240
DB 181 ROTGMMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNNNGIYGFQFMREGAK 240
QY 241 SLWRGNGINVLKIAPESAIKFMAVEQIKRLVGSDOETLRIHERLVAGSLAGAIQSSIYP 300
DB 241 SLWRGNGINVLKIAPESAIKFMAVEQIKRLVGSDOETLRIHERLVAGSLAGAIQSSIYP 300
QY 301 MEVLKTRMALRKQYSGMLDCARRILAREGVAAPYKGYVPMGLIIPYAGIDILAVETL 360
DB 301 MEVLKTRMALRKQYSGMLDCARRILAREGVAAPYKGYVPMGLIIPYAGIDILAVETL 360
QY 361 KNNMLQYVANSADPGVFVLLACGTSSSTCGQLASYPALVTRTMOQAISREGAPEVTMS 420
DB 361 KNNMLQYVANSADPGVFVLLACGTSSSTCGQLASYPALVTRTMOQAISREGAPEVTMS 420
QY 421 SLFKHILRTGAFGLYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR 469
DB 421 SLFKHILRTGAFGLYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR 469
RESULT 4
Q705K2 PRELIMINARY; PRT; 469 AA.
AC Q705K2;
DB 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mitochondrial ATP-Mg/Pi carrier (Small calcium-binding mitochondrial carrier 2).
GN Name=SLC25A25; Synonym=SCAMC-2;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=15123600; DOI=10.1074/jbc.M400445200;
RA Piermonte G., De Leonardi F., Todisco S., Palmieri L., Lasorsa F.M., Palmieri F.;
RT "Identification of the mitochondrial ATP-Mg/Pi transporter: Bacterial expression, reconstitution, functional characterization and tissue

RT distribution.";
RL J. Biol. Chem. 279:30722-30730 (2004).
RN 12;
RP SEQUENCE FROM N.A.
RX PubMed=15054102; DOI=10.1074/jbc.M401417200;
RA del Arco A., Satriategui J.;
RT "Identification of a novel human subfamily of mitochondrial carriers with calcium-binding domains.";
RL J. Biol. Chem. 279:24701-24713 (2004).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; AJ61963; CA04060.1; -.
DR HSSP; O64537; 1A55.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002113; Aden_translocator.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_Like.
DR InterPro; IPR002167; Graves_DC.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00036; ehand; 3.
DR Pfam; PF00153; Mito_carr; 3.
DR PRINTS; PR00927; ADPTRNSLCASE.
DR PRINTS; PR00928; GRAVESDC.
DR PRINTS; PR00926; MITOCARRIER.
DR PRODOM; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 3.
DR PROSITE; PS50920; SOLCAR; 3.
DR Transmembrane; Transport.
KW SEQUENCE 489 AA; 54638 MW; 1BD8AAB1C40592DB CRC64;
Query Match 88.5%; Score 2144; DB 2; Length 489;
Best Local Similarity 99.0%; Pred. No. 2.2e-123;
Matches 416; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 50 QWKQKIYQAGDQDLQDLQDLFEFVHYLDHHEKRLVFKILDKKNDGRIDAQELMQSLRD 109
DB 70 QFPKXIVQAGDQDLQDLQDLFEFVHYLDHHEKRLVFKSLDKKNDGRIDAQELMQSLRD 129
QY 110 LGYKISEQQAEEKILKSMKNGTMTIDNEMRDYHLHPVENIPETILYWKSTIPDVGEN 169
DB 130 LGYKISEQQAEEKILKSMKNGTMTIDNEMRDYHLHPVENIPETILYWKSTIPDVGEN 189
QY 170 LTPDEFTVEERQTGMMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNNMGIVGG 229
DB 190 LTPDEFTVEERQTGMMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNNMGIVGG 249
QY 230 FTQMIREGARSILWRGNGINVLKIAPESAIKFMAVEQIKRLVGSDOETLRIHERLVAGSL 289
DB 250 FTQMIREGARSILWRGNGINVLKIAPESAIKFMAVEQIKRLVGSDOETLRIHERLVAGSL 309
QY 290 AGAIAQSSIVPEVLKTRMALRKQYSGMLDCARRILAREGVAAPYKGYVPMGLIIPY 349
DB 310 AGAIAQSSIVPEVLKTRMALRKQYSGMLDCARRILAREGVAAPYKGYVPMGLIIPY 369
QY 350 AGIDILAVETLKNAMLOHYVANSADPGVFVLLACGTSSSTCGQLASYPALVTRTMOQA 409
DB 370 AGIDILAVETLKNAMLOHYVANSADPGVFVLLACGTSSSTCGQLASYPALVTRTMOQA 429
QY 410 SIEGAPEVTMSLFLKHILRTGAFGLYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR 469
DB 430 SIEGAPEVTMSLFLKHILRTGAFGLYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR 489
RESULT 5
Q6KCM6 PRELIMINARY; PRT; 503 AA.
AC Q6KCM6;
DB 06KCM6;
DT 06KCM6;
RT expression, reconstitution, functional characterization and tissue

```
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Small calcium-binding mitochondrial carrier 2.
GN Name=SCMC-2;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15054102; DOI=10.1074/jbc.M401417200;
RA del Arco A., Satriategui J.;
RT "Identification of a novel human subfamily of mitochondrial carriers
RT with calcium-binding domains."
RL J. Biol. Chem. 279:24701-24713(2004).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; AB619990; CAF04496.1; -.
DR HSSP; P02586; 1A2X.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002113; Aden. transloc.
DR InterPro; IPR010983; EF_Hand.
DR InterPro; IPR002167; Graves_DC.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PRO0927; ADPTNSLCASE.
DR PRINTS; PRO0928; GRAVESDC.
DR PRINTS; PRO0928; MITOCARIER.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS50920; SOLCAR; 3.
DR Transmembrane; Transport.
SQ SEQUENCE 503 AA; 55397 MW; 01F0C668941DA37F CRC64;

Query Match 88.4%; Score 2143; DB 2; Length 503;
Best Local Similarity 99.8%; Pred. No. 2.6e-123;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 53 OKIVQAGDDLDQQLDFEEFVHYLDQHEKKRLVFKILDKNGRIDAOEIMSLDGLV 112
DB 87 OKIVQAGDDLDQQLDFEEFVHYLDQHEKKRLVFKSLDKNGRIDAOEIMOSLRDLGV 146
QY 113 KISEQQAEEKILKSMKNGTWTIDNEMRDYHLHPVENIPEIILYMGHSTIPVGENLTV 172
DB 147 KISEQQAEEKILKSMKNGTWTIDNEMRDYHLHPVENIPEIILYMGHSTIPVGENLTV 206
QY 173 PDEFYVEERQTGMWHRHLVAGGAGAVSRTCTAPLDRLKVLQVHA SRNNMGIVGGFTQ 232
DB 207 PDEFYVEERQTGMWHRHLVAGGAGAVSRTCTAPLDRLKVLQVHA SRNNMGIVGGFTQ 266
QY 233 MIREGARSIMRNGINVLKIAPESAIKFMAVEOIRIVGSDOETRIHERLVAAGSLAG 292
DB 267 MIREGARSIMRNGINVLKIAPESAIKFMAVEOIRIVGSDOETRIHERLVAAGSLAG 336
QY 293 IAOSSIYPMVEVLKTRMALRKGTQYSGMLDCARRILAREGVAAYFKYGVPMMLGIIPYAGI 352
DB 327 IAOSSIYPMVEVLKTRMALRKGTQYSGMLDCARRILAREGVAAYFKYGVPMMLGIIPYAGI 386
QY 353 DLAVETTLKNAVLQHYAVNSADPGVFULLACGTMSSTCGQLASYPALAVTRMQAASIE 412
DB 387 DLAVETTLKNAVLQHYAVNSADPGVFULLACGTMSSTCGQLASYPALAVTRMQAASIE 446
QY 413 GAPEVTMSLFFGHIILTEGAFGLYRGLAPFMKVIYAVSISYVYENLKTITLGVQR 469
DB 447 GAPEVTMSLFFGHIILTEGAFGLYRGLAPFMKVIYAVSISYVYENLKTITLGVQR 503
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RESULT 6
ID Q96P21 PRELIMINARY; PRT; 568 AA.
AC Q96P21;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Small calcium-binding mitochondrial carrier 2.
GN Name=KIAA1896;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins."
RL DNA Res. 8:179-187(2001).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; AB067483; BAB67789.1; -.
DR HSSP; P02588; 1TNX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR010983; EF_Hand.
DR InterPro; IPR002048; EF_Hand.
DR InterPro; IPR002167; Graves_DC.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00036; efhand; 2.
DR Pfam; PF00153; Mitc_carri; 3.
DR PRINTS; PRO0928; GRAVESDC.
DR PRINTS; PRO0928; MITOCARIER.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS50920; SOLCAR; 3.
DR Transmembrane; Transport.
SQ SEQUENCE 568 AA; 63578 MW; 81A02DCD8CE74B8 CRC64;

Query Match 87.6%; Score 2123; DB 2; Length 568;
Best Local Similarity 96.1%; Pred. No. 5e-122;
Matches 415; Conservative 2; Mismatches 3; Indels 12; Gaps 1;

QY 50 OKMKIVQAGDDLDQQLDFEEFVHYLDQHEKKRLVFKILDKNGRIDAOEIMSLD 109
DB 137 OKMKIVQAGDDLDQQLDFEEFVHYLDQHEKKRLVFKSLDKNGRIDAOEIMOSLRDL 196
QY 110 LGVYKISEQQAEEKILKIRGTFMGFPTVMDKNGTWTIDNEMRDYHLHPVENIPEIILY 157
DB 197 LGVYKISEQQAEEKILKIRGTFMGFPTVMDKNGTWTIDNEMRDYHLHPVENIPEIILY 256
QY 197 LGVYKISEQQAEEKILKIRGTFMGFPTVMDKNGTWTIDNEMRDYHLHPVENIPEIILY 256
DB 197 LGVYKISEQQAEEKILKIRGTFMGFPTVMDKNGTWTIDNEMRDYHLHPVENIPEIILY 256
QY 158 WKHSTIPDVGENITVDEFTVEERQTGMWHRHLVAGGAGAVSRTCTAPLDRLKVLQV 217
DB 257 WKHSTIPDVGENITVDEFTVEERQTGMWHRHLVAGGAGAVSRTCTAPLDRLKVLQV 316
QY 218 ASRSNNMGIVGGFTQWIRREGARSIMRNGINVLKIAPESAIKFMAVEOIRIVGSDOET 277
DB 317 ASRSNNMGIVGGFTQWIRREGARSIMRNGINVLKIAPESAIKFMAVEOIRIVGSDOET 376
QY 278 LRHERLVAAGSLAGAIQAOSSIYPMVEVLKTRMALRKGTQYSGMLDCARRILAREGVAAYFK 337
DB 377 LRHERLVAAGSLAGAIQAOSSIYPMVEVLKTRMALRKGTQYSGMLDCARRILAREGVAAYFK 436
QY 338 GYVPMMLGIIPYAGIDLAVETTLKNAVLQHYAVNSADPGVFULLACGTMSSTCGQLASYP 397
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DB 437 GYPMNLGIFPYAGIDAVETLKNMLOGYRANVNSDPGVLLACTMSTCGQLASYP 496
 QY 398 LALVTRMQOASIEGAEVETMSSLFPHILIRTEGAFGLYGLAENFKVIPAVISYVY 457
 DB 497 LALVTRMQOASIEGAEVETMSSLFPHILIRTEGAFGLYGLAENFKVIPAVISYVY 556
 QY 458 ENKITLGVQSR 469
 DB 557 ENKITLGVQSR 568
 RESULT 7
 Q8BHGO
 ID Q8BHGO PRELIMINARY; PRT; 502 AA.
 AC Q8BHGO;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
 DE library, clone: C43003103 product: weakly similar to PEROXISOMAL CA-
 DE DEPENDENT SOLUTE CARRIER (Mus musculus ES cells cDNA, RIKEN full-
 DE length enriched library, clone: C330055N23 product: weakly similar to
 DE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER).
 GN Name=SLOC25a25;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA The FANTOM Consortium.
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 RL [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh N.,
 RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Iehi Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Koude M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Yasunishi M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Iehi Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Koude M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Yasunishi M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL; AK049392; BAC3730.1; -;
 DR EMBL; AK082756; BAC38604.1; -;
 DR HSSP; P02588; ITNX.
 DR MGD; MGI:1915913; SLOC25a25.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005743; C: mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F: binding; IEA.
 DR GO; GO:0005509; F: calcium ion binding; IEA.
 DR GO; GO:0006810; P: transport; IEA.
 DR InterPro; IPR02048; EF-hand.
 DR InterPro; IPR010983; EF-hand like.
 DR InterPro; IPR02167; Graves_DC.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR02067; Mlt_carrier.
 DR Pfam; PF00036; efhand; 4.
 DR Pfam; PF00153; Mito_carr; 3.
 DR PRINTS; PR00926; GRAVESDC.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRODOM; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFN; 4.
 DR PROSITE; PSS0920; SOLCAR; 3.
 KW Transmembrane; Transport.
 SO SEQUENCE 502 AA; 55287 MW; 21ABC9B940B361FE CRC64;
 QY Query Match 86.5%; Score 2096; DB 2; Length 502;
 DB Best Local Similarity 97.4%; Pred. No. 2e-120;
 DB Matches 406; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 53 QKTVAGDRLDQDLPDEFVHYLQDEKRLRVFKLIDKNGRIDAOEIMOSLRIGV 112
 DB 86 KTVAGDRLDQDLPDEFVHYLQDEKRLRVFKLIDKNGRIDAOEIMOSLRIGV 145
 QY 113 KISEQAEKILKMDKNGTITIMNEWRDYLHPENIPEILLYMGHSTIPDGENILTV 172
 DB 146 KISEQAEKILKMDKNGTITIMNEWRDYLHPENIPEILLYMGHSTIPDGENILTV 205
 QY 173 PDEFVTEEROTGMWRHLVAGGAGAVSRTCTAPLDRKLVMOVHASRSNNMGIVGFTQ 232
 DB 206 PDEFVTEEROTGMWRHLVAGGAGAVSRTCTAPLDRKLVMOVHASRSNNMGIVGFTQ 265
 QY 233 MIBEGGARSIMRNGINVLKIPBSAIPMAVYQIKRLVSDDETLRIHERLVAGSLAGA 292

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Db      266 MIREGAKSLMRNGINVLKIAPESAIKFMAVQMKRLVSDDETHRIHRLVAGSILAGA 325
Qy      293 IAOSIYPMFVLKTRMALRKTCGYSGLDCARRILAREGVAAPFKYVPMNLGIIPYAGI 352
Db      326 IAOSIYPMFVLKTRMALRKTCGYSGLDCARRILAREGVAAPFKYVPMNLGIIPYAGI 365
Qy      353 DIAVETLKXNAMLQHYAVNSADPGVFLVLLACGTMSSTCGQLASVPLALVETRMQAQASIE 412
Db      386 DIAVETLKXNAMLQHYAVNSADPGVFLVLLACGTMSSTCGQLASVPLALVETRMQAQASIE 445
Qy      413 GAEVUMSSIFKHILITREGAFGLYRGILAPFMKVIIPAVSISYVYENLKITLIGVQR 469
Db      446 GAEVUMSSIFKHILITREGAFGLYRGILAPFMKVIIPAVSISYVYENLKITLIGVQR 502

RESULT 8
06NKM8
ID 06NKM8      PRELIMINARY;      PRT;      501 AA.
AC 06NKM8;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE 110030N17R1K protein.
GN Name=110030N17R1K;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.;
RA Klausner R.D.; Collins F.S.; Wagner R.H.; Shemen C.M.; Schlier G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.T.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusik K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Donald M.F.; Casavant T.L.; Schaefer T.E.;
RA Brownstein M.J.; Ueda T.B.; Tohiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Lonnellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McSwan P.J.; McKernan K.J.; Malek J.A.; Gutarane P.H.;
RA Richards S.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.V.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.C.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Whiting M.; Madan A.; Young A.C.; Madan A.; Rodriguez S.; Sanchez A.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska J.; Smalusz D.E.; Schnerch A.; Schein J.E.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
EMBL: BC066988; AF066988.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005743; C: mitochondrial inner membrane; IEA.
DR GO: GO:0005488; F: binding; IEA.
DR GO: GO:0005509; F: calcium ion binding; IEA.
DR GO: GO:0005215; F: transporter activity; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR002113; Aden_tns1ctof.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR010983; EF_Hand_1like.
DR InterPro: IPR002167; Graves DC.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; MLC_carrier.
DR Pfam: PF00036; ehand; 2.

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DR Pfam; PF00153; Mito_carr; 3.
DR PRINTS; PR00927; ADPTRNSLCASE.
DR PRINTS; PR00928; GRAVEDSC.
DR PRINTS; PR00926; MITOCARRIER.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS0920; SOLCAR; 3.
KW Transmembrane; Transport.
SQ SEQUENCE 501 AA; 56077 MW; 7FCC4FB5B8977778 CRC64;

Query Match      85.9%; Score 2082; DB 2; Length 501;
Best Local Similarity 87.5%; Pred. No. 1,4e-119;
Matches 414; Conservative 13; Mismatches 28; Indels 18; Gaps 2;

Qy      9 PVIEAQTEPEFYESKGLPAELKSIKLVFIPISQEFSTYRQMKIVQAGDLDGOLD 68
Db      35 PARGDQMTTLGQNGRAETKRPILLVVGABQF-----PKTIQAQGDLDGOLD 88
Qy      69 FEEFVHYLDHEKKRLVFKILDKNDGRIDAEIWSLRDLGVKISEQAEEKILKS--- 125
Db      89 FEEFVHYLDHEKKRLVFKILDKNDGRIDAEIWSLRDLGVKISEQAEEKILKRI 148
Qy      126 -----MDKGMNTIMNEMRDYHLHPVENIPEIILYWGKSTIPDVGMLTVPDER 176
Db      149 GHFWGPVTTYMDKNGTWTIDMNEWRDYHLHPVENIPEIILYWGKSTIPDVGMLTVPDER 208
Qy      177 TYBERQTGMWRRHLVAGGAGVSRCTAPLDRLKYLQVHASRNNMGIVGFTQWIRE 236
Db      209 TYBERQTGMWRRHLVAGGAGVSRCTAPLDRLKYLQVHASRNNMGIVGFTQWIRE 268
Qy      237 GGAISLMRGNGINVLKIAPESAIKFMAVQMKRLVSDDETHRIHRLVAGSILAGA 296
Db      269 GGAISLMRGNGINVLKIAPESAIKFMAVQMKRLVSDDETHRIHRLVAGSILAGA 328
Qy      297 SIYPMFVLKTRMALRKTCGYSGLDCARRILAREGVAAPFKYVPMNLGIIPYAGI 356
Db      329 SIYPMFVLKTRMALRKTCGYSGLDCARRILAREGVAAPFKYVPMNLGIIPYAGI 388
Qy      357 YETLKXNAMLQHYAVNSADPGVFLVLLACGTMSSTCGQLASVPLALVETRMQAQASIGAPE 416
Db      389 YETLKXNAMLQHYAVNSADPGVFLVLLACGTMSSTCGQLASVPLALVETRMQAQASIGAPE 448
Qy      417 VTMSSIFKHILITREGAFGLYRGILAPFMKVIIPAVSISYVYENLKITLIGVQR 469
Db      449 VTMSSIFKHILITREGAFGLYRGILAPFMKVIIPAVSISYVYENLKITLIGVQR 501

RESULT 9
080T78
ID 080T78      PRELIMINARY;      PRT;      515 AA.
AC 080T78;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE NKIA1896 protein (Fragment).
GN Name=SLC25A25; Synonyms=NKIA1896;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N.; Kikuno R.; Ohara R.; Inamoto S.; Aizawa H.; Yuasa S.;
RA Nakajima D.; Nagase T.; Ohara O.; Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene;
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 10:35-48(2003).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
EMBL: AK125568; BAC65850.1; -.

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatcenco L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshlyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Holik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skelton U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strauberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; BC066404; AA66404.1; -
DR ZFIN; ZDB-GENE-040426-2396; zgc:77454.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002113; Aden_translocor.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF-hand like.
DR InterPro; IPR002167; Graves DC.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mito_carrier.
DR Pfam; PF00153; Mito_carr; 3.
DR Pfam; PF00153; Mito_carr; 3.
DR PRINTS; PR00927; ADPTRNSLCASR.
DR PRINTS; PR00928; GRAVESDC.
DR PRINTS; PR00926; MITOCARRIER.
DR Prodom; PD000012; EF-hand; 1.
DR PROSITE; PS50920; SOLCAR; 3.
DR Transmembrane; Transport.
SQ SEQUENCE 469 AA; 52457 MW; 7F583A75FA61BEE CRC64;
Query Match 78.2%; Score 1895; DB 2; Length 469;
Best Local Similarity 75.7%; Pred. No. 3,8e-108;
Matches 355; Conservative 54; Mismatches 60; Indels 0; Gaps 0;
QY 1 MLCGLVYVIGAEQTFQYFESKGLPAELKSLFELSVFIPSOEFSTYRQMKIVQAGD 60
DB 1 MLCGLVYVYVHNSQIEVEYFESNGLPSELKSLKSLVSLPQSFSTRARRKKSLSKTEB 60
QY 61 KDLDSQIDFEFFVYLDQHEKKLVKILDKKDKRIDAOELIQSLDLGVKISQOAE 120
DB 61 KEHQGDQDFEFVYLDQHEKDLKLVFKSMRKIAGQVNNADINYSIRLDGVHLSLQAE 120
QY 121 KIILSKMKGKMTIDMNBMRDYLHLHPVENIPETILYWKSTIPDVGENTLVPEFTYEE 180
DB 121 KIILSKMKGKMTIDMNBMRDYLHLHPVENIPETILYWKSTIPDVGESLWVPEFTVEE 180
QY 181 ROTGMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNNNGIVGGFTOMIREGAR 240
DB 181 HLTGMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNNNGIVGGFTOMIREGAR 240
QY 241 SLRNGNINVLKIPESAIKMAVEQIKRLVGSQOETLRIRHERLVAGSLAGAIQSSITP 300
DB 241 SLRNGNINVLKIPESAIKMAVEQIKRLVGSQOETLRIRHERLVAGSLAGAIQSSITP 300
QY 301 MEVLKTRMALRKTOYSGMLDCARRILAREGVAAFYKGYVNMGIIPYAGIDLAAYETL 360
DB 301 MEVLKTRMALRKTOYSGMLDCARRILAREGVAAFYKGYVNMGIIPYAGIDLAAYETL 360

DB 301 MEVLKTRMALRKTOYSGMLDCARRILAREGVAAFYKGYVNMGIIPYAGIDLAAYETL 360
QY 361 KNAWLQHYAVNSADPGFVLLACGTMSSTGQLASYPALVTRTMOQAISLEGAPETMS 420
DB 361 KNAWLQHYAVNSADPGFVLLACGTMSSTGQLASYPALVTRTMOQAISLEGAPETMS 420
QY 421 SLPGHIRTGAFGLYGLAPNPMKVPVAVSIVYVENIKITLGVOSR 469
DB 421 SLPGHIRTGAFGLYGLAPNPMKVPVAVSIVYVENIKITLGVOSR 469
RESULT 13
ID 06KCM4 PRELIMINARY; PRT; 366 AA.
AC 06KCM4;
RT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Small calcium-binding mitochondrial carrier 2.
GN Name=SCAMC-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15054102; DOI=10.1074/jbc.M401417200;
RA del Arco A., Salustegui J.;
RT "Identification of a novel human subfamily of mitochondrial carriers
RT with calcium-binding domains."
RL J. Biol. Chem. 279:24701-24713(2004).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; AJ619992; CA04498.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002113; Aden_translocor.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF-hand like.
DR InterPro; IPR002167; Graves DC.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mito_carrier.
DR Pfam; PF00153; Mito_carr; 3.
DR PRINTS; PR00927; ADPTRNSLCASR.
DR PRINTS; PR00928; GRAVESDC.
DR PRINTS; PR00926; MITOCARRIER.
DR Prodom; PD000012; EF-hand; 1.
DR PROSITE; PS50920; SOLCAR; 3.
DR Transmembrane; Transport.
SQ SEQUENCE 366 AA; 40589 MW; C02B524BE6120F90 CRC64;
Query Match 77.8%; Score 1886; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 MSLRLDGVKISQOAEKILKSMDKNGTMTIDNNEWDYHLHPVENIPETILYWKSTI 163
DB 1 MSLRLDGVKISQOAEKILKSMDKNGTMTIDNNEWDYHLHPVENIPETILYWKSTI 163
QY 164 FDVGENTLVPEFTVEERQGMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNN 223
DB 164 FDVGENTLVPEFTVEERQGMWRHLVAGGAGAVSRCTAPLDRLKVLMOVHASRNN 223
QY 224 MGIVGGFTOMIREGARSLRNGNINVLKIPESAIKMAVEQIKRLVGSQOETLRIRHER 283
DB 224 MGIVGGFTOMIREGARSLRNGNINVLKIPESAIKMAVEQIKRLVGSQOETLRIRHER 283
QY 284 LVAGSLAGAIQSSITPMEVLKTRMALRKTOYSGMLDCARRILAREGVAAFYKGYVNM 343
DB 284 LVAGSLAGAIQSSITPMEVLKTRMALRKTOYSGMLDCARRILAREGVAAFYKGYVNM 343
QY 343 MEVLKTRMALRKTOYSGMLDCARRILAREGVAAFYKGYVNM 360
DB 343 MEVLKTRMALRKTOYSGMLDCARRILAREGVAAFYKGYVNM 360

QY 344 LGIIPVAGIDLAVYETLKNAMLOHYAVNSADPGVFLVLLACGTMSSTCGOLASYPALVLT 403
DB 241 LGIIPVAGIDLAVYETLKNAMLOHYAVNSADPGVFLVLLACGTMSSTCGOLASYPALVLT 300
QY 404 RMOQASIEEAPPEVTMSLFFKHILRTGAGLRYGLAPNPKVLPANVISYVYENLKIT 463
DB 301 RMOQASIEEAPPEVTMSLFFKHILRTGAGLRYGLAPNPKVLPANVISYVYENLKIT 360
QY 464 LGVQSR 469
DB 361 LGVQSR 366
RESULT 14
Q8VB14 PRELIMINARY; PRT; 366 AA.
AC Q8VB14
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE 110030N17R1k protein.
GN Name=SLC25A25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney, and Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Manisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez Y., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: Belongs to the mitochondrial carrier family.
DR EMBL; BC022114; AAH22114.1; -
DR EMBL; BC019978; AAH19978.1; -
DR MGI; MGI:1915913; SLC25A25.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00153; Mito_carr; 3.
DR PRINTS; PR00928; GRAVESDC.
DR PRINTS; PR00926; MITOCHRIER.

DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PSS0920; SOLCAR; 3.
KW Transmembrane; Transport.
SQ SEQUENCE 366 AA; 40633 MW; 1F691F6FE507617 CRC64;
Query Match 76.1%; Score 1843; DB 2; Length 366;
Best Local Similarity 97.5%; Pred. No. 4,5e-105;
Matches 357; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 104 MOSLRDVGKISSEQQAELIKSMKDKGTMTIDNENRMDYHLHPVENIPETIIYWKSTI 163
DB 1 MOSLRDVGKISSEQQAELIKSMKDKGTMTIDNENRMDYHLHPVENIPETIIYWKSTI 60
QY 164 FDVGENLTVDEFTVEERQTGMWRHLVAGGAGAVSRCTAPDLRLKVLMOYHARSNN 223
DB 61 FDVGENLTVDEFTVEERQTGMWRHLVAGGAGAVSRCTAPDLRLKVLMOYHARSNN 120
QY 224 MGIVGFTQWIRREGGAKSLMRGNGINVLKTAPESAIKFMAVEQIKLVGSDQETLRHER 283
DB 121 MCIVGFTQWIRREGGAKSLMRGNGINVLKTAPESAIKFMAVEQIKLVGSDQETLRHER 180
QY 284 LVAGSLAGATQSSIYPMETLKTMRMLRKTGQSGMDCARILLAREGVAAPKGYVPM 343
DB 181 LVAGSLAGATQSSIYPMETLKTMRMLRKTGQSGMDCARILLAREGVAAPKGYVPM 240
QY 344 LGIIPVAGIDLAVYETLKNAMLOHYAVNSADPGVFLVLLACGTMSSTCGOLASYPALVLT 403
DB 241 LGIIPVAGIDLAVYETLKNAMLOHYAVNSADPGVFLVLLACGTMSSTCGOLASYPALVLT 300
QY 404 RMOQASIEEAPPEVTMSLFFKHILRTGAGLRYGLAPNPKVLPANVISYVYENLKIT 463
DB 301 RMOQASIEEAPPEVTMSLFFKHILRTGAGLRYGLAPNPKVLPANVISYVYENLKIT 360
QY 464 LGVQSR 469
DB 361 LGVQSR 366
RESULT 15
Q9BSA6 PRELIMINARY; PRT; 308 AA.
AC Q9BSA6
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE MCSC protein (Fragment).
GN Name=MCSC;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Manisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez Y., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL; BC005163; AA005163.2;
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002113; Adu_nucleo.
 DR InterPro; IPR002167; Graves_DC.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; Mitc_carr_3.
 DR PRINTS; PR00927; ADPTRSLCASE.
 DR PRINTS; PR00928; GRAVESDC.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS50920; SOLCAR; 3.
 KM Transmembrane; Transport.
 FT NON_TER 1
 SQ SEQUENCE 308 AA; 3654 MW; C75DAC2F473D3EE4 CRC64;

Query Match 64.6%; Score 1566; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 3.5e-88;
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 IFDVGENTLYPDEFTVEREQGMWRLVAGGAGAVSRCTAPLDRLKVLMOVHASRN 222
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 DB 2 IFDVGENTLYPDEFTVEREQGMWRLVAGGAGAVSRCTAPLDRLKVLMOVHASRN 61
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 QY 223 NMGI VGGFTQMIREGARSILRGNGINVLKIPESAIKFMAYEQIKRLVGSDOETLR IHE 282
 |||||
 DB 62 NMGI VGGFTQMIREGARSILRGNGINVLKIPESAIKFMAYEQIKRLVGSDOETLR IHE 121
 |||||
 QY 283 RLVAGSLAGAIAGSSIYPMEVLTCTRMALRTGTQYSGMLDCARRILAREGVAAFYKGYVPN 342
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 DB 122 RLVAGSLAGAIAGSSIYPMEVLTCTRMALRTGTQYSGMLDCARRILAREGVAAFYKGYVPN 181
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 QY 343 MLGIIIPYAGIDLAYETLKNAMLQHYAVNSADPGVFVLLACGTMSSTCGQLASTPLALVR 402
 |||||
 DB 182 MLGIIIPYAGIDLAYETLKNAMLQHYAVNSADPGVFVLLACGTMSSTCGQLASTPLALVR 241
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 QY 403 TRMQAASISGAPVETMSLPEKHLIRTEGAFGLYRGLAPNEMKVIIPAVSISVYVENLKI 462
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 DB 242 TRMQAASISGAPVETMSLPEKHLIRTEGAFGLYRGLAPNEMKVIIPAVSISVYVENLKI 301
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 QY 463 TLGVQSR 469
 |||||
 DB 302 TLGVQSR 308

Search completed: August 5, 2005, 20:33:53
 Job time : 207 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 20:20:50 ; Search time 25 Seconds

(Without alignments)
1400.416 Million cell updates/sec

Title: US-10-063-565-58

Perfect score: 2423
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	2362	97.5	469 3 US-09-188-930-339	Sequence 339, App
2	2362	97.5	469 4 US-09-312-283C-339	Sequence 339, App
3	1588	65.5	312 3 US-09-188-930-142	Sequence 142, App
4	1588	65.5	312 4 US-09-312-283C-142	Sequence 142, App
5	682.5	28.2	376 4 US-09-270-767-44809	Sequence 44809, A
6	427.5	17.6	289 4 US-09-796-766-20	Sequence 20, App1
7	418.5	17.3	433 4 US-09-796-766-14	Sequence 18, App1
8	417	17.2	272 4 US-09-796-766-18	Sequence 18, App1
9	415.5	17.1	436 4 US-09-796-766-21	Sequence 21, App1
10	354	14.6	142 4 US-09-270-767-43371	Sequence 43371, A
11	354	14.6	142 4 US-09-270-767-58719	Sequence 58719, A
12	347.5	14.3	410 4 US-09-796-766-10	Sequence 10, App1
13	318.5	13.1	227 4 US-09-270-767-32789	Sequence 32789, A
14	318.5	13.1	227 4 US-09-270-767-48006	Sequence 48006, A
15	318.5	13.1	259 4 US-09-248-796A-11339	Sequence 20733, A
16	314	13.0	288 4 US-09-434-354-49	Sequence 43571, A
17	314	13.0	288 4 US-09-709-785-49	Sequence 43571, A
18	313	12.9	328 3 US-09-068-140A-15	Sequence 45, App1
19	307	12.7	307 4 US-09-248-796A-17597	Sequence 15, App1
20	304.5	12.6	304 4 US-09-949-016-11339	Sequence 11339, A
21	304	12.5	297 4 US-09-434-354-47	Sequence 47, App1
22	304	12.5	297 4 US-09-709-785-47	Sequence 47, App1
23	302.5	12.5	320 4 US-08-933-750C-12	Sequence 12, App1
24	302.5	12.5	320 4 US-09-234-613-12	Sequence 12, App1
25	302.5	12.5	330 4 US-09-976-594-711	Sequence 711, App1
26	302	12.5	298 3 US-08-961-871-10	Sequence 10, App1
27	302	12.5	298 4 US-09-434-354-48	Sequence 48, App1

28	302	12.5	298 4 US-09-709-785-48	Sequence 48, App1
29	299.5	12.4	289 3 US-09-068-140A-10	Sequence 10, App1
30	298.5	12.3	301 4 US-09-248-796A-20731	Sequence 20733, A
31	289	11.9	302 4 US-09-270-767-33858	Sequence 33858, A
32	289	11.9	302 4 US-09-270-767-49075	Sequence 49075, A
33	289	11.9	322 4 US-09-949-016-8722	Sequence 8722, Ap
34	289	11.9	322 4 US-09-949-016-8723	Sequence 8723, Ap
35	286	11.6	335 4 US-09-482-373-118	Sequence 118, App
36	280.5	11.6	328 4 US-09-248-796A-15301	Sequence 15301, A
37	277	11.4	250 4 US-09-743-847-2	Sequence 2, App1
38	272	11.2	220 4 US-09-796-766-4	Sequence 2, App1
39	270.5	11.2	678 4 US-09-949-016-6406	Sequence 4606, Ap
40	270.5	11.2	685 4 US-09-949-016-11180	Sequence 11180, A
41	268.5	11.1	306 4 US-09-248-796A-17738	Sequence 17738, A
42	268	11.1	125 3 US-08-505-223-320	Sequence 320, App
43	265.5	11.0	221 4 US-09-501-558-2	Sequence 2, App1
44	261	10.8	674 3 US-09-160-119-2	Sequence 2, App1
45	253.5	10.5	364 4 US-09-870-113-2	Sequence 2, App1
46	245	10.1	309 4 US-10-001-051B-2	Sequence 51, App1
47	242	10.0	309 1 US-08-518-878B-51	Sequence 51, App1
48	242	10.0	309 2 US-08-807-861A-51	Sequence 51, App1
49	242	10.0	309 2 US-08-470-868A-51	Sequence 51, App1
50	242	10.0	309 3 US-09-210-681-51	Sequence 51, App1
51	242	10.0	309 3 US-08-946-719A-51	Sequence 51, App1
52	242	10.0	309 4 US-09-547-983-51	Sequence 51, App1
53	242	10.0	309 4 US-09-743-847-4	Sequence 4, App1
54	242	10.0	337 4 US-09-949-016-9410	Sequence 9410, Ap
55	241	9.9	309 4 US-10-009-962-8	Sequence 8, App1
56	239.5	9.9	299 1 US-08-518-878B-56	Sequence 56, App1
57	239.5	9.9	299 2 US-08-470-868A-56	Sequence 56, App1
58	237.5	9.8	351 2 US-08-933-750C-19	Sequence 19, App1
59	237.5	9.8	351 3 US-09-234-613-19	Sequence 19, App1
60	236	9.7	312 3 US-09-142-565-2	Sequence 2, App1
61	236	9.7	312 4 US-09-808-457-2	Sequence 2, App1
62	236	9.7	312 4 US-09-423-410-4	Sequence 4, App1
63	236	9.7	312 4 US-10-009-962-9	Sequence 9, App1
64	234	9.7	447 3 US-09-160-119-4	Sequence 4, App1
65	232.5	9.6	320 4 US-09-248-796A-17608	Sequence 17608, A
66	231	9.5	422 2 US-08-937-466-4	Sequence 4, App1
67	231	9.5	422 2 US-09-172-528-4	Sequence 4, App1
68	231	9.5	432 3 US-09-318-199-4	Sequence 4, App1
69	231	9.5	432 3 US-09-503-579-4	Sequence 4, App1
70	228	9.4	308 2 US-08-937-466-2	Sequence 2, App1
71	228	9.4	308 2 US-09-172-528-2	Sequence 2, App1
72	228	9.4	308 3 US-09-318-199-2	Sequence 2, App1
73	228	9.4	308 3 US-09-503-579-2	Sequence 2, App1
74	226.5	9.3	381 4 US-09-248-796A-15499	Sequence 15499, A
75	226.5	9.3	310 4 US-09-743-847-5	Sequence 5, App1
76	225.5	9.3	307 4 US-09-743-847-3	Sequence 3, App1
77	225.5	9.3	309 4 US-09-949-016-10401	Sequence 10401, A
78	225	9.3	316 4 US-09-248-796A-17731	Sequence 17731, A
79	224.5	9.3	367 4 US-09-248-796A-14830	Sequence 14830, A
80	224.5	9.3	289 4 US-09-248-796A-17636	Sequence 17636, A
81	223.5	9.2	358 4 US-09-370-767-44738	Sequence 44738, A
82	223.5	9.1	366 5 PCT-US94-09799-1	Sequence 1, App1
83	220	9.0	314 4 US-09-248-796A-17612	Sequence 17612, A
84	217.5	9.0	265 4 US-10-009-962-7	Sequence 7, App1
85	217.5	9.0	307 4 US-09-870-113-8	Sequence 8, App1
86	215.5	8.9	617 4 US-09-248-796A-17637	Sequence 17637, A
87	216.5	8.9	288 4 US-09-248-796A-17637	Sequence 17637, A
88	215.5	8.9	288 4 US-09-248-796A-17637	Sequence 17637, A
89	213	8.8	365 4 US-09-270-767-43637	Sequence 43637, A
90	208.5	8.6	301 4 US-09-949-016-6885	Sequence 6885, Ap
91	208.5	8.6	311 2 US-08-775-009-3	Sequence 3, App1
92	208.5	8.6	333 4 US-09-949-016-9952	Sequence 9952, Ap
93	208	8.6	291 4 US-09-248-796A-20693	Sequence 20693, A
94	207	8.5	293 4 US-09-501-558-4	Sequence 4, App1
95	205	8.5	377 4 US-09-949-016-10067	Sequence 10067, A
96	205	8.5	377 4 US-09-949-016-10068	Sequence 10068, A
97	204	8.4	368 4 US-09-949-016-8818	Sequence 8818, Ap
98	201.5	8.3	307 2 US-08-807-861A-56	Sequence 56, App1
99	201.5	8.3	307 3 US-09-210-681-56	Sequence 56, App1
100	201.5	8.3	307 3 US-08-946-719A-56	Sequence 56, App1

101	201.5	8.3	307	4	US-09-547-983-56	Sequence 56, Appl1	174	128	5.3	416	4	US-09-989-025A-8	Sequence 8, Appl1
102	199	8.2	275	4	US-09-808-457-4	Sequence 4, Appl1	175	127	5.2	45	4	US-09-270-767-60276	Sequence 60276, A
103	199	8.2	275	4	US-09-423-410-6	Sequence 6, Appl1	176	126	5.2	142	1	US-07-951-715A-24	Sequence 24, Appl1
104	199	8.2	306	4	US-10-009-962-5	Sequence 5, Appl1	177	126	5.2	142	2	US-08-459-448A-24	Sequence 24, Appl1
105	196.5	8.1	311	2	US-08-775-009-32	Sequence 32, Appl1	178	126	5.2	142	3	US-08-459-595A-24	Sequence 24, Appl1
106	196	8.1	303	1	US-08-518-878A-37	Sequence 37, Appl1	179	126	5.2	142	3	US-08-459-504B-24	Sequence 24, Appl1
107	196	8.1	303	1	US-08-294-522B-36	Sequence 36, Appl1	180	126	5.2	142	3	US-08-459-444-24	Sequence 24, Appl1
108	196	8.1	303	2	US-08-807-861A-37	Sequence 37, Appl1	181	126	5.2	142	3	US-09-547-422-24	Sequence 24, Appl1
109	196	8.1	303	2	US-08-470-868A-37	Sequence 37, Appl1	182	126	5.2	142	4	US-09-988-462-24	Sequence 24, Appl1
110	196	8.1	303	3	US-09-210-681-37	Sequence 37, Appl1	183	125.5	5.2	404	4	US-09-248-796A-20715	Sequence 20715, A
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112	196	8.1	303	4	US-09-547-983-37	Sequence 37, Appl1	185	123.5	5.1	163	2	US-08-698-805-8	Sequence 8, Appl1
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114	194.5	8.0	355	4	US-09-463-239-30	Sequence 30, Appl1	187	123	5.1	152	3	US-08-963-409-5	Sequence 5, Appl1
115	193.5	8.0	230	4	US-09-248-796A-20827	Sequence 20827, A	188	123	5.1	152	3	US-09-949-016-6600	Sequence 6600, Ap
116	193	8.0	309	4	US-09-270-767-41737	Sequence 41737, A	189	122	5.0	149	3	US-08-963-409-3	Sequence 3, Appl1
117	193	8.0	313	4	US-09-248-796A-17621	Sequence 17621, A	190	121.5	5.0	169	3	US-08-720-625-4	Sequence 4, Appl1
118	192	7.9	225	4	US-09-489-847-155	Sequence 155, Ap	191	121.5	5.0	170	3	US-08-764-563-5	Sequence 5, Appl1
119	192	7.9	316	4	US-10-009-962-6	Sequence 6, Appl1	192	121	5.0	226	4	US-09-248-796A-17599	Sequence 17599, A
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122	189.5	7.8	256	3	US-09-318-199-6	Sequence 6, Appl1	195	119	4.9	652	2	US-08-818-253-4	Sequence 4, Appl1
123	189.5	7.8	256	3	US-09-503-579-6	Sequence 6, Appl1	196	119	4.9	652	3	US-08-818-252-4	Sequence 4, Appl1
124	189.5	7.8	256	3	US-09-248-796A-17601	Sequence 17601, A	197	118.5	4.9	157	4	US-09-270-767-42776	Sequence 42776, A
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129	176.5	7.3	258	4	US-10-009-962-4	Sequence 4, Appl1	202	116	4.8	208	2	US-09-096-082-1	Sequence 1, Appl1
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131	167	6.9	350	4	US-09-248-796A-17746	Sequence 17746, A	204	116	4.8	256	3	US-09-298-731-36	Sequence 36, Appl1
132	166.5	6.9	239	4	US-09-248-796A-17746	Sequence 20814, A	205	116	4.8	256	4	US-09-350-614-36	Sequence 36, Appl1
133	163.5	6.7	134	4	US-09-270-767-33795	Sequence 33795, A	206	116	4.8	642	2	US-08-818-252-6	Sequence 6, Appl1
134	163.5	6.7	154	4	US-09-270-767-49012	Sequence 49012, A	207	116	4.8	642	2	US-08-818-252-6	Sequence 6, Appl1
135	159.5	6.6	201	4	US-09-248-796A-15943	Sequence 15943, A	208	116	4.8	656	2	US-08-818-252-8	Sequence 8, Appl1
136	159	6.6	301	4	US-09-215-694-13	Sequence 13, Appl1	209	116	4.8	656	3	US-08-818-252-8	Sequence 8, Appl1
137	158	6.5	102	4	US-09-248-796A-20734	Sequence 16428, A	210	115.5	4.8	191	3	US-08-655-352-5	Sequence 5, Appl1
138	151.5	6.3	371	4	US-09-463-239-35	Sequence 35, Appl1	211	115.5	4.8	191	3	US-08-655-352-6	Sequence 5, Appl1
139	151	6.2	299	4	US-09-599-360B-91	Sequence 91, Appl1	212	115.5	4.8	191	3	US-09-258-016-6	Sequence 6, Appl1
140	150.5	6.2	308	4	US-09-599-360B-91	Sequence 91, Appl1	213	115.5	4.8	191	3	US-09-258-016-6	Sequence 6, Appl1
141	150.5	6.2	308	2	US-08-602-941-1	Sequence 2, Appl1	214	115.5	4.8	191	4	US-09-257-825B-6	Sequence 6, Appl1
142	147.5	6.1	160	2	US-08-602-941-1	Sequence 1, Appl1	215	115.5	4.8	191	4	US-09-257-825B-6	Sequence 6, Appl1
143	147.5	6.1	160	3	US-08-961-264-1	Sequence 1, Appl1	216	115.5	4.8	207	4	US-09-949-016-9875	Sequence 9875, Ap
144	147.5	6.1	160	4	US-09-442-099A-1	Sequence 1, Appl1	217	115	4.7	188	3	US-09-949-016-9875	Sequence 3, Appl1
145	147.5	6.1	160	4	US-09-612-342-1	Sequence 1, Appl1	218	115	4.7	229	3	US-09-399-913-70	Sequence 70, Appl1
146	147.5	6.1	160	4	US-09-612-421A-1	Sequence 1, Appl1	219	115	4.7	229	4	US-09-350-614-70	Sequence 70, Appl1
147	147.5	6.1	160	4	US-09-949-016-6336	Sequence 6336, Ap	220	115	4.7	223	3	US-09-399-913-49	Sequence 49, Appl1
148	147.5	6.1	160	4	US-09-949-016-6336	Sequence 10343, A	221	115	4.7	223	3	US-09-350-614-49	Sequence 49, Appl1
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152	143	5.9	166	4	US-09-270-767-48917	Sequence 2, Appl1	225	113.5	4.7	181	4	US-07-951-715A-21	Sequence 21, Appl1
153	139	5.7	150	3	US-09-239-909-2	Sequence 10989, A	226	113	4.7	408	2	US-08-459-448A-21	Sequence 21, Appl1
154	138	5.7	164	4	US-09-949-016-10989	Sequence 2, Appl1	227	113	4.7	408	2	US-08-459-448A-21	Sequence 21, Appl1
155	138	5.7	247	4	US-09-368-819A-2	Sequence 4, Appl1	228	113	4.7	408	3	US-08-459-595A-21	Sequence 21, Appl1
156	138	5.7	247	4	US-09-368-819A-2	Sequence 4, Appl1	229	113	4.7	408	3	US-08-459-504B-21	Sequence 21, Appl1
157	137.5	5.7	330	1	US-08-993-380-4	Sequence 2, Appl1	230	113	4.7	408	3	US-08-459-444-21	Sequence 21, Appl1
158	137.5	5.7	149	1	US-08-100-874-2	Sequence 2, Appl1	231	113	4.7	408	3	US-09-547-422-21	Sequence 21, Appl1
159	137.5	5.7	203	3	US-09-270-767-61255	Sequence 61255, A	232	113	4.7	408	4	US-09-988-462-21	Sequence 21, Appl1
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161	134	5.5	187	4	US-09-248-796A-20529	Sequence 20529, A	234	113	4.7	464	2	US-08-459-448A-22	Sequence 22, Appl1
162	134	5.5	287	4	US-09-248-796A-15613	Sequence 15613, A	235	113	4.7	464	3	US-08-459-595A-22	Sequence 22, Appl1
163	133.5	5.5	179	3	US-08-764-563-4	Sequence 4, Appl1	236	113	4.7	464	3	US-08-459-504B-22	Sequence 22, Appl1
164	133	5.5	145	3	US-08-720-625-5	Sequence 5, Appl1	237	113	4.7	464	3	US-08-459-444-22	Sequence 0, Appl1
165	132.5	5.5	112	4	US-09-796-766-2	Sequence 2, Appl1	238	113	4.7	464	3	US-09-447-422-22	Sequence 0, Appl1
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169	128	5.3	149	3	US-08-641-873-20	Sequence 20, Appl1	242	112	4.6	256	4	US-09-350-614-32	Sequence 32, Appl1
170	128	5.3	149	4	US-09-513-999C-7913	Sequence 7913, Ap	243	112	4.6	259	4	US-09-949-016-10093	Sequence 10093, A
171	128	5.3	149	4	US-09-949-016-6770	Sequence 6770, Ap	244	111.5	4.6	188	4	US-09-270-767-44075	Sequence 44075, A
172	128	5.3	184	4	US-09-949-016-7507	Sequence 7507, Ap	245	111	4.6	92	4	US-09-248-796A-17600	Sequence 17600, A
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248	111	4.6	434	1	US-08-453-654-5	Sequence 5, Appli	321	101.5	4.2	270	3	US-09-399-913-18	Sequence 18, Appli
249	111	4.6	434	1	US-08-453-655B-5	Sequence 5, Appli	322	101.5	4.2	270	3	US-09-298-731-18	Sequence 18, Appli
250	111	4.6	434	3	US-08-453-652-5	Sequence 5, Appli	323	101.5	4.2	270	3	US-09-350-614-18	Sequence 18, Appli
251	111	4.6	434	3	US-08-449-731-5	Sequence 7, Appli	324	101.5	4.2	463	1	US-07-951-715A-25	Sequence 25, Appli
252	110.5	4.6	191	3	US-08-655-352-7	Sequence 7, Appli	325	101.5	4.2	463	2	US-08-459-448A-25	Sequence 25, Appli
253	110.5	4.6	191	3	US-09-258-016-7	Sequence 7, Appli	326	101.5	4.2	463	3	US-08-459-595A-25	Sequence 25, Appli
254	110.5	4.6	191	4	US-09-257-825B-7	Sequence 7, Appli	327	101.5	4.2	463	3	US-08-459-504B-25	Sequence 25, Appli
255	110.5	4.6	1551	4	US-09-437-568A-46	Sequence 46, Appli	328	101.5	4.2	463	3	US-08-459-444-25	Sequence 0, Appli
256	110	4.5	134	4	US-09-503-191A-2	Sequence 2, Appli	329	101.5	4.2	463	3	US-09-547-422-25	Sequence 0, Appli
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259	109	4.5	234	4	US-09-248-796A-18332	Sequence 18332, A	332	101	4.2	200	1	US-08-764-051-3	Sequence 3, Appli
260	108	4.5	155	4	US-09-270-767-4776	Sequence 44776, A	333	101	4.2	211	4	US-09-356-778-1	Sequence 1, Appli
261	108	4.5	186	3	US-08-655-352-8	Sequence 8, Appli	334	101	4.2	226	4	US-09-949-016-11107	Sequence 11107, A
262	108	4.5	186	3	US-09-258-016-8	Sequence 8, Appli	335	101	4.2	515	4	US-09-107-332A-6214	Sequence 6214, Ap
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264	108	4.5	195	4	US-09-949-016-10220	Sequence 10220, A	337	100.5	4.1	225	3	US-09-298-731-30	Sequence 30, Appli
265	108	4.5	216	3	US-09-399-913-2	Sequence 2, Appli	338	100.5	4.1	225	4	US-09-350-614-30	Sequence 30, Appli
266	108	4.5	216	3	US-09-399-913-6	Sequence 6, Appli	339	100.5	4.1	225	4	US-09-399-913-22	Sequence 22, Appli
267	108	4.5	216	3	US-09-298-731-2	Sequence 2, Appli	340	100.5	4.1	252	3	US-09-399-913-28	Sequence 28, Appli
268	108	4.5	216	3	US-09-298-731-6	Sequence 6, Appli	341	100.5	4.1	252	3	US-09-399-913-42	Sequence 42, Appli
269	108	4.5	216	4	US-09-350-614-2	Sequence 2, Appli	342	100.5	4.1	252	3	US-09-298-731-22	Sequence 22, Appli
270	108	4.5	216	4	US-09-350-614-6	Sequence 6, Appli	343	100.5	4.1	252	3	US-09-298-731-28	Sequence 28, Appli
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272	108	4.5	227	3	US-09-399-913-10	Sequence 10, Appli	345	100.5	4.1	252	4	US-09-350-614-28	Sequence 28, Appli
273	108	4.5	227	3	US-09-298-731-8	Sequence 8, Appli	346	100.5	4.1	252	4	US-09-350-614-42	Sequence 42, Appli
274	108	4.5	227	3	US-09-298-731-10	Sequence 10, Appli	347	100.5	4.1	257	3	US-09-399-913-16	Sequence 16, Appli
275	108	4.5	227	4	US-09-350-614-8	Sequence 8, Appli	348	100.5	4.1	257	3	US-09-298-731-16	Sequence 16, Appli
276	108	4.5	227	4	US-09-350-614-10	Sequence 10, Appli	349	100.5	4.1	257	4	US-09-350-614-16	Sequence 16, Appli
277	108	4.5	245	3	US-09-399-913-4	Sequence 4, Appli	350	100.5	4.1	303	3	US-09-247-155-107	Sequence 107, App
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280	107	4.4	84	4	US-09-270-767-56984	Sequence 56984, A	353	100	4.1	203	3	US-09-399-913-12	Sequence 12, Appli
281	107	4.4	89	4	US-09-437-568A-48	Sequence 48, Appli	354	100	4.1	203	3	US-09-298-731-12	Sequence 12, Appli
282	106.5	4.4	220	3	US-09-399-913-24	Sequence 24, Appli	355	100	4.1	266	3	US-09-350-614-12	Sequence 12, Appli
283	106.5	4.4	220	3	US-09-399-913-26	Sequence 26, Appli	356	100	4.1	266	3	US-09-350-614-12	Sequence 12, Appli
284	106.5	4.4	220	3	US-09-298-731-24	Sequence 24, Appli	357	100	4.1	266	4	US-09-350-614-12	Sequence 12, Appli
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287	106.5	4.4	220	4	US-09-350-614-26	Sequence 26, Appli	360	99.5	4.1	174	1	US-08-328-322-17	Sequence 17, Appli
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290	106.5	4.4	252	4	US-09-350-614-20	Sequence 20, Appli	363	99	4.1	151	3	US-09-425-665-2	Sequence 2, Appli
291	106.5	4.4	270	3	US-09-399-913-14	Sequence 14, Appli	364	99	4.1	151	3	US-09-685-668-2	Sequence 2, Appli
292	106.5	4.4	270	3	US-09-298-731-14	Sequence 14, Appli	365	98.5	4.1	91	4	US-09-621-976-4470	Sequence 4470, Ap
293	106.5	4.4	270	4	US-09-350-614-14	Sequence 14, Appli	366	98.5	4.1	95	3	US-09-142-565-6	Sequence 6, Appli
294	106.5	4.4	281	4	US-09-949-016-8244	Sequence 8244, Ap	367	98.5	4.1	131	4	US-09-621-976-4204	Sequence 4204, Ap
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297	106	4.4	248	4	US-09-802-633-1	Sequence 1, Appli	370	98.5	4.1	1005	4	US-09-949-016-6391	Sequence 6391, Ap
298	105	4.3	639	3	US-09-347-801-17	Sequence 17, Appli	371	98	4.0	484	4	US-09-198-452A-732	Sequence 732, Ap
299	105	4.3	639	4	US-09-854-731-17	Sequence 17, Appli	372	98	4.0	495	4	US-09-438-185A-694	Sequence 694, Ap
300	104.5	4.3	225	4	US-09-270-767-44807	Sequence 44807, A	373	97.5	4.0	1031	4	US-09-914-259-24	Sequence 24, Appli
301	103.5	4.3	135	1	US-08-468-853-4	Sequence 4, Appli	374	97	4.0	2472	4	US-09-538-092-1312	Sequence 1312, Ap
302	103.5	4.3	135	1	US-08-468-855-4	Sequence 4, Appli	375	96.5	4.0	200	3	US-09-298-731-32	Sequence 32, Appli
303	103.5	4.3	135	1	US-08-310-357-4	Sequence 4, Appli	376	96.5	4.0	910	4	US-09-107-532A-6533	Sequence 6533, Ap
304	103.5	4.3	135	2	US-08-468-852-4	Sequence 4, Appli	377	96	4.0	268	2	US-08-338-059A-9	Sequence 9, Appli
305	103.5	4.3	135	2	US-08-468-857-4	Sequence 4, Appli	378	96	4.0	268	3	US-09-157-349-9	Sequence 9, Appli
306	103.5	4.3	146	3	US-08-963-409-1	Sequence 1, Appli	379	96	4.0	666	4	US-09-107-532A-5205	Sequence 5205, Ap
307	103.5	4.3	146	4	US-10-031-403B-1	Sequence 1, Appli	380	95.5	3.9	149	4	US-09-270-767-45884	Sequence 45884, A
308	103.5	4.3	191	1	US-08-766-605-3	Sequence 3, Appli	381	95.5	3.9	189	1	US-08-684-682-4	Sequence 4, Appli
309	103.5	4.3	191	2	US-09-094-812-3	Sequence 3, Appli	382	95.5	3.9	189	2	US-09-096-082-4	Sequence 4, Appli
310	103.5	4.3	191	4	US-09-538-092-1178	Sequence 1178, Ap	383	95.5	3.9	189	4	US-09-949-016-7734	Sequence 7734, Ap
311	103.5	4.3	1270	4	US-09-902-540-14299	Sequence 14299, A	384	95.5	3.9	199	4	US-09-949-016-7894	Sequence 7894, Ap
312	103	4.3	172	4	US-09-285-601-2	Sequence 2, Appli	385	95.5	3.9	252	3	US-09-251-645-13	Sequence 13, Appli
313	103	4.3	172	4	US-09-949-016-6450	Sequence 6450, Ap	386	95	3.9	815	4	US-09-538-092-1196	Sequence 1196, Ap
314	103	4.3	172	4	US-09-949-016-10275	Sequence 10275, A	387	94.5	3.9	193	4	US-09-949-016-6181	Sequence 6181, Ap
315	102	4.2	74	3	US-09-142-565-4	Sequence 4, Appli	388	94.5	3.9	456	1	US-08-464-164-2	Sequence 2, Appli
316	102	4.2	198	4	US-09-538-092-1045	Sequence 1045, Ap	389	94.5	3.9	456	2	US-08-338-057-2	Sequence 2, Appli
317	102	4.2	202	1	US-08-820-051-1	Sequence 1, Appli	390	94.5	3.9	456	2	US-08-668-416-2	Sequence 2, Appli
318	102	4.2	202	4	US-09-949-016-7318	Sequence 7318, Ap	391	94	3.9	196	3	US-09-048-889-1	Sequence 1, Appli
319	101.5	4.2	193	4	US-09-870-113-4	Sequence 4, Appli	392	94	3.9	220	2	US-08-840-683-8	Sequence 8, Appli

393	94	3.9	317	2	US-08-555-722-8	Sequence 8, Appl1	466	88	3.6	3074	4	US-09-543-681A-5508	Sequence 5508, Ap
394	94	3.9	317	3	US-09-384-301-8	Sequence 8, Appl1	467	87.5	3.6	126	4	US-09-513-999C-7982	Sequence 7982, Ap
395	94	3.9	339	4	US-09-949-016-10766	Sequence 10766, A	468	87.5	3.6	222	4	US-09-949-016-9547	Sequence 9547, Ap
396	94	3.9	382	4	US-10-130-792A-2	Sequence 2, Appl1	469	87.5	3.6	233	3	US-09-399-913-51	Sequence 51, Appl
397	94	3.9	383	4	US-09-252-991A-18162	Sequence 18162, A	470	87.5	3.6	233	4	US-09-350-614-51	Sequence 51, Appl
398	94	3.9	411	4	US-09-248-796A-18197	Sequence 18197, A	471	87.5	3.6	347	4	US-09-461-325-277	Sequence 277, App
399	94	3.9	133	4	US-09-257-825B-2	Sequence 2, Appl1	472	87.5	3.6	347	4	US-10-012-542-277	Sequence 277, App
400	93.5	3.9	535	3	US-08-369-822C-24	Sequence 24, Appl1	473	87.5	3.6	347	4	US-10-115-123-227	Sequence 277, App
401	93.5	3.9	535	3	US-08-582-776C-39	Sequence 39, Appl1	474	87.5	3.6	522	4	US-09-949-016-7549	Sequence 7549, Ap
402	93.5	3.9	535	3	US-08-434-831B-36	Sequence 36, Appl1	475	87.5	3.6	607	4	US-09-438-185A-565	Sequence 565, App
403	93	3.8	189	1	US-08-884-682-3	Sequence 3, Appl1	476	87	3.6	344	4	US-09-489-039A-8488	Sequence 8488, Ap
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406	93	3.8	704	4	US-09-902-540-10479	Sequence 10479, A	479	87	3.6	534	4	US-09-198-452A-217	Sequence 217, App
407	93	3.8	7257	3	US-09-335-409-5	Sequence 5, Appl1	480	87	3.6	540	4	US-09-438-185A-200	Sequence 200, App
408	93	3.8	7257	3	US-09-568-102-5	Sequence 5, Appl1	481	87	3.6	540	4	US-09-588-995A-115	Sequence 115, App
409	93	3.8	7257	3	US-09-567-969-5	Sequence 5, Appl1	482	87	3.6	757	4	US-09-622-880B-1	Sequence 1, Appl1
410	93	3.8	7257	3	US-09-568-480-5	Sequence 5, Appl1	483	87	3.6	821	4	US-09-308-345A-48	Sequence 48, Appl1
411	93	3.8	7257	3	US-09-568-486-5	Sequence 5, Appl1	484	87	3.6	821	4	US-09-622-880B-15	Sequence 15, Appl1
412	93	3.8	7257	3	US-09-568-472-5	Sequence 5, Appl1	485	87	3.6	899	4	US-09-538-092-27	Sequence 27, Appl1
413	93	3.8	7257	3	US-09-567-899-5	Sequence 5, Appl1	486	87	3.6	1489	6	5183745-2	Patent No. 5183745
414	92.5	3.8	133	3	US-08-655-352-2	Sequence 2, Appl1	487	87	3.6	1489	6	5183745-2	Patent No. 5183745
415	92.5	3.8	133	3	US-09-258-016-2	Sequence 2, Appl1	488	87	3.6	1706	3	US-08-669-785-2	Sequence 2, Appl1
416	92	3.8	133	3	US-08-655-352-4	Sequence 4, Appl1	489	87	3.6	1794	6	5183745-6	Patent No. 5183745
417	92	3.8	133	3	US-09-258-016-4	Sequence 4, Appl1	490	87	3.6	1794	6	5183745-6	Patent No. 5183745
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420	92	3.8	3080	6	5223423-4	Patent No. 5223423	493	86.5	3.6	325	2	US-09-626-499-4	Sequence 2, Appl1
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422	91.5	3.8	315	2	US-08-910-927B-3	Sequence 3, Appl1	495	86.5	3.6	325	4	US-09-284-926-2	Sequence 4, Appl1
423	91.5	3.8	315	3	US-09-270-870-3	Sequence 3, Appl1	496	86.5	3.6	401	4	US-09-598-995A-91	Sequence 91, Appl1
424	91.5	3.8	315	4	US-10-164-595-12	Sequence 12, Appl1	497	86.5	3.6	401	4	US-09-598-995A-91	Sequence 91, Appl1
425	91.5	3.8	315	4	US-10-164-595-61	Sequence 61, Appl1	498	86.5	3.6	540	3	US-08-461-722-4	Sequence 4, Appl1
426	91.5	3.8	588	1	US-08-391-615-5	Sequence 5, Appl1	499	86.5	3.6	540	3	US-08-336-251-4	Sequence 4, Appl1
427	91	3.8	133	3	US-08-655-352-3	Sequence 3, Appl1	500	86.5	3.6	540	4	US-09-468-041-4	Sequence 4, Appl1
428	91	3.8	133	3	US-09-258-016-3	Sequence 3, Appl1	501	86.5	3.6	540	4	US-09-613-303-4	Sequence 4, Appl1
429	91	3.8	133	3	US-09-257-825B-3	Sequence 3, Appl1	502	86.5	3.6	540	4	US-10-267-311-4	Sequence 4, Appl1
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431	91	3.8	543	4	US-09-602-787A-212	Sequence 212, App	504	86.5	3.6	540	4	US-09-809-745-1	Sequence 1, Appl1
432	91	3.8	630	4	US-09-485-529-1	Sequence 1, Appl1	505	86.5	3.6	540	5	PCT-US94-06362-29	Sequence 4, Appl1
433	91	3.8	925	4	US-09-540-236-3586	Sequence 3586, Ap	506	86.5	3.6	648	4	US-09-613-303-2	Sequence 29, Appl1
434	90.5	3.7	70	4	US-09-270-767-32409	Sequence 32409, A	507	86.5	3.6	648	4	US-10-267-311-29	Sequence 29, Appl1
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436	90.5	3.7	177	4	US-09-248-796A-15300	Sequence 15300, A	509	86.5	3.6	3224	2	US-08-705-660-34	Sequence 34, Appl1
437	90.5	3.7	168	4	US-09-270-767-43188	Sequence 43188, A	510	86.5	3.6	3224	4	US-08-989-045-34	Sequence 34, Appl1
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441	90	3.7	460	4	US-09-489-039A-10519	Sequence 10519, A	514	86	3.5	331	2	US-08-910-927B-5	Sequence 5, Appl1
442	90	3.7	518	4	US-09-248-796A-19845	Sequence 19845, A	515	86	3.5	331	3	US-09-270-270-5	Sequence 5, Appl1
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444	90	3.7	1705	3	US-08-669-785-4	Sequence 4, Appl1	517	86	3.5	331	4	US-09-661-403-11	Sequence 11, Appl1
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447	89.5	3.7	639	4	US-09-613-303-17	Sequence 17, Appl1	520	86	3.5	517	4	US-09-248-796A-16950	Sequence 16950, A
448	89.5	3.7	139	4	US-10-267-311-17	Sequence 17, Appl1	521	86	3.5	534	4	US-09-949-016-10320	Sequence 10320, A
449	89	3.7	139	4	US-09-270-767-33651	Sequence 33651, A	522	86	3.5	534	4	US-08-187-793-4	Sequence 4, Appl1
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451	89	3.7	202	1	US-07-804-894-1	Sequence 1, Appl1	524	86	3.5	604	4	US-09-591-095-18	Sequence 18, Appl1
452	89	3.7	202	1	US-08-419-102-1	Sequence 1, Appl1	525	86	3.5	673	3	US-09-423-439-32	Sequence 32, Appl1
453	89	3.7	543	2	US-08-776-597A-2	Sequence 2, Appl1	526	86	3.5	673	3	US-09-423-439-32	Sequence 32, Appl1
454	89	3.7	543	2	US-08-693-228-2	Sequence 2, Appl1	527	86	3.5	1022	1	US-09-489-039A-9290	Sequence 9290, Ap
455	89	3.7	543	2	US-08-693-228-2	Sequence 2, Appl1	528	86	3.5	1022	1	US-08-771-364A-8	Sequence 8, Appl1
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457	88.5	3.7	564	4	US-09-198-452A-601	Sequence 601, App	530	85.5	3.5	218	4	US-09-328-352-7752	Sequence 7752, Ap
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462	88	3.6	483	4	US-09-134-000C-4862	Sequence 4862, Ap	535	85.5	3.5	611	4	US-08-709-731A-2	Sequence 2, Appl1
463	88	3.6	700	4	US-09-308-345A-46	Sequence 46, Appl1	536	85.5	3.5	937	1	US-08-253-155A-31	Sequence 31, Appl1
464	88	3.6	821	3	US-09-422-869-24	Sequence 24, Appl1	537	85.5	3.5	937	1	US-09-538-092-1052	Sequence 1052, Ap
465	88	3.6	821	4	US-09-538-092-972	Sequence 972, App	538	85.5	3.5	959	4	US-09-538-092-1091	Sequence 1091, Ap

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540	85	3.5	446	4	US-09-134-000C-3894	Sequence 3894, Ap	613	82	3.4	335	3	US-08-798-096-10	Sequence 10, Appli
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543	85	3.5	869	4	US-09-830-433A-42	Sequence 42, Appli	616	82	3.4	335	4	US-08-553-125A-10	Sequence 10, Appli
544	85	3.5	1104	3	US-09-268-347-28	Sequence 28, Appli	617	82	3.4	335	4	US-10-114-464-10	Sequence 10, Appli
545	85	3.5	1104	3	US-09-268-347-28	Sequence 34, Appli	618	82	3.4	335	4	US-09-290-586A-21	Sequence 21, Appli
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551	84.5	3.5	381	4	US-09-134-000C-5229	Sequence 5229, Ap	624	82	3.4	906	4	US-09-328-352-6037	Sequence 6037, Ap
552	84.5	3.5	517	4	US-09-252-991A-29696	Sequence 29696, A	625	82	3.4	918	2	US-08-568-983-14	Sequence 14, Appli
553	84.5	3.5	517	4	US-09-257-825B-21	Sequence 21, Appli	626	82	3.4	2457	2	US-08-568-976-14	Sequence 14, Appli
554	84.5	3.5	710	4	US-09-540-236-5557	Sequence 3557, Ap	627	82	3.4	4968	4	US-09-252-991A-25671	Sequence 25671, A
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558	84.5	3.5	1093	3	US-09-538-092-701	Sequence 701, App	631	81.5	3.4	53	4	US-09-270-767-46898	Sequence 46898, A
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561	84	3.5	335	5	PCT-US95-13820-6	Sequence 6, Appli	634	81.5	3.4	335	4	US-09-252-991A-31381	Sequence 31381, A
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564	84	3.5	698	4	US-09-710-279-2388	Sequence 2388, Ap	637	81.5	3.4	343	1	US-08-187-793-2	Sequence 2, Appli
565	84	3.5	734	4	US-09-252-991A-19106	Sequence 19106, A	638	81.5	3.4	331	1	US-08-178-257-6	Sequence 6, Appli
566	84	3.5	809	4	US-09-248-796A-19668	Sequence 19668, A	639	81.5	3.4	417	1	US-07-649-591B-7	Sequence 7, Appli
567	84	3.5	905	3	US-09-134-001C-3782	Sequence 3782, Ap	640	81.5	3.4	417	1	US-08-277-540-7	Sequence 7, Appli
568	83.5	3.4	261	4	US-09-134-000C-4019	Sequence 4019, Ap	641	81.5	3.4	417	1	US-08-430-787A-7	Sequence 7, Appli
569	83.5	3.4	356	2	US-08-461-990B-2	Sequence 2, Appli	642	81.5	3.4	460	4	US-09-949-016-7994	Sequence 7994, Ap
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572	83.5	3.4	948	1	US-08-698-551-14	Sequence 1, Appli	645	81.5	3.4	540	2	US-08-368-834-20	Sequence 20, Appli
573	83.5	3.4	948	2	US-08-602-228-14	Sequence 14, Appli	646	81.5	3.4	541	2	US-08-467-822-34	Sequence 34, Appli
574	83.5	3.4	948	2	US-08-533-901B-14	Sequence 14, Appli	647	81.5	3.4	541	2	US-08-447-154-19	Sequence 19, Appli
575	83.5	3.4	948	2	US-08-839-032A-14	Sequence 14, Appli	648	81.5	3.4	541	3	US-08-432-697-34	Sequence 34, Appli
576	83.5	3.4	948	2	US-08-839-031A-14	Sequence 14, Appli	649	81.5	3.4	541	3	US-08-466-248-34	Sequence 34, Appli
577	83.5	3.4	948	3	US-09-185-258C-14	Sequence 14, Appli	650	81.5	3.4	559	2	US-08-756-317-10	Sequence 10, Appli
578	83.5	3.4	948	5	PCT-US95-12724-14	Sequence 14, Appli	651	81.5	3.4	559	2	US-09-091-609-4	Sequence 4, Appli
579	83.5	3.4	965	4	US-09-252-991A-24038	Sequence 24038, A	652	81.5	3.4	582	3	US-09-419-459-2	Sequence 2, Appli
580	83.5	3.4	1083	4	US-09-328-352-5493	Sequence 5493, Ap	653	81.5	3.4	708	3	US-08-235-836C-76	Sequence 76, Appli
581	83.5	3.4	2183	2	US-08-348-891A-7	Sequence 7, Appli	654	81.5	3.4	1019	1	US-08-271-364A-7	Sequence 7, Appli
582	83.5	3.4	2183	2	US-08-905-817-7	Sequence 7, Appli	655	81.5	3.4	1019	2	US-08-222-715B-26	Sequence 26, Appli
583	83.5	3.4	3033	1	US-07-925-695-9	Sequence 9, Appli	656	81.5	3.4	5215	3	US-09-105-537-2	Sequence 2, Appli
584	83	3.4	287	4	US-09-621-976-5547	Sequence 5547, Ap	657	81	3.3	356	4	US-09-949-016-7951	Sequence 7951, Ap
585	83	3.4	394	3	US-09-328-352-5087	Sequence 5087, Ap	658	81	3.3	416	4	US-09-583-110-3878	Sequence 3878, Ap
586	83	3.4	394	3	US-09-134-001C-4954	Sequence 4954, Ap	659	81	3.3	446	4	US-09-602-787A-602	Sequence 602, App
587	83	3.4	860	3	US-08-092-817-4	Sequence 4, Appli	660	81	3.3	610	4	US-09-710-279-482	Sequence 482, App
588	83	3.4	860	3	US-08-485-128-4	Sequence 4, Appli	661	81	3.3	614	3	US-09-134-001C-3061	Sequence 3061, Ap
589	83	3.4	860	4	US-09-804-778A-8	Sequence 8, Appli	662	81	3.3	744	2	US-08-177-109A-2	Sequence 2, Appli
590	83	3.4	1055	2	US-08-659-251-5	Sequence 4, Appli	663	81	3.3	764	2	US-08-687-706-2	Sequence 2, Appli
591	83	3.4	1055	2	US-08-659-251-5	Sequence 5, Appli	664	81	3.3	788	4	US-09-949-016-11021	Sequence 11021, A
592	83	3.4	1055	3	US-09-256-490-5	Sequence 5, Appli	665	81	3.3	820	4	US-09-583-110-4219	Sequence 4219, A
593	83	3.4	1055	5	PCT-US9C-11445-5	Sequence 5, Appli	666	81	3.3	834	4	US-09-107-433-4760	Sequence 4760, Ap
594	83	3.4	1410	2	US-08-470-058-4	Sequence 4, Appli	667	81	3.3	903	1	US-08-021-601-12	Sequence 12, Appli
595	83	3.4	1410	2	US-09-037-188-4	Sequence 4, Appli	668	81	3.3	903	1	US-08-082-849B-12	Sequence 12, Appli
596	83	3.4	1410	3	US-09-285-310-4	Sequence 4, Appli	669	81	3.3	1032	3	PCT-US94-01624-12	Sequence 26, Appli
597	83	3.4	138	4	US-09-902-540-12842	Sequence 12842, A	670	81	3.3	81	3	US-09-914-259-26	Sequence 26, Appli
598	82.5	3.4	336	4	US-09-583-110-4759	Sequence 4759, Ap	671	81	3.3	1032	4	US-09-538-092-1293	Sequence 1293, Ap
599	82.5	3.4	468	4	US-09-902-540-13234	Sequence 13234, A	672	81	3.3	1368	4	US-09-967-908A-2	Sequence 2, Appli
600	82.5	3.4	531	4	US-09-248-796A-15957	Sequence 15957, A	673	81	3.3	1368	4	US-10-159-151-2	Sequence 2, Appli
601	82.5	3.4	744	3	US-09-738-884-4	Sequence 4, Appli	674	80.5	3.3	112	4	US-09-248-796A-20732	Sequence 20732, A
602	82.5	3.4	744	3	US-10-096-961A-4	Sequence 4, Appli	675	80.5	3.3	158	4	US-09-949-016-10439	Sequence 10439, A
603	82.5	3.4	1234	4	US-09-489-039A-8741	Sequence 8741, Ap	676	80.5	3.3	187	4	US-09-949-016-6721	Sequence 6721, Ap
604	82.5	3.4	4545	2	US-08-804-227C-14	Sequence 14, Appli	677	80.5	3.3	226	4	US-09-270-767-45534	Sequence 45534, A
605	82.5	3.4	4550	2	US-08-804-327C-8	Sequence 8, Appli	678	80.5	3.3	305	4	US-09-339-159B-18	Sequence 18, Appli
606	82.5	3.4	4550	2	US-08-804-198-2	Sequence 2, Appli	679	80.5	3.3	333	4	US-09-237-119-2	Sequence 18, Appli
607	82	3.4	146	4	US-09-270-767-33612	Sequence 33612, A	680	80.5	3.3	330	4	US-09-252-991A-17923	Sequence 17923, A
608	82	3.4	335	1	US-08-208-007A-10	Sequence 10, Appli	681	80.5	3.3	335	4	US-09-252-991A-31961	Sequence 31961, A
609	82	3.4	335	1	US-09-120-365-56	Sequence 66, Appli	682	80.5	3.3	336	4	US-09-198-452A-662	Sequence 662, App
610	82	3.4	335	3	US-09-515-039-56	Sequence 66, Appli	683	80.5	3.3	359	1	US-08-137-627-4	Sequence 4, Appli
611	82	3.4	335	3	US-08-860-255A-6	Sequence 6, Appli	684	80.5	3.3	359	2	US-08-865-348-4	Sequence 4, Appli

685	80.5	3.3	478	4	US-09-252-991A-19678	Sequence 19678, A	758	79	3.3	790	4	US-09-543-681A-5847	Sequence 5847, Ap
686	80.5	3.3	543	4	US-09-252-991A-30375	Sequence 30375, A	759	79	3.3	801	4	US-09-913-301-7	Sequence 7, Appl1
687	80.5	3.3	548	2	US-08-467-822-31	Sequence 31, Appl	760	79	3.3	868	4	US-09-543-681A-5357	Sequence 5357, Ap
688	80.5	3.3	548	3	US-08-432-697-31	Sequence 31, Appl	761	79	3.3	1212	4	US-09-252-991A-26616	Sequence 26616, A
689	80.5	3.3	548	3	US-08-466-248-31	Sequence 31, Appl	762	79	3.3	1276	4	US-09-949-016-8886	Sequence 6886, Ap
690	80.5	3.3	585	4	US-09-462-951B-1	Sequence 1, Appl1	763	79	3.3	2037	3	US-09-306-998-3	Sequence 3, Appl1
691	80.5	3.3	655	1	US-07-736-178C-2	Sequence 2, Appl1	764	79	3.3	2476	4	US-09-824-574-7	Sequence 7, Appl1
692	80.5	3.3	814	4	US-09-252-991A-22923	Sequence 22923, A	765	79	3.3	2662	4	US-09-595-684B-31	Sequence 31, Appl1
693	80.5	3.3	944	4	US-09-107-532A-4864	Sequence 4864, Ap	766	79	3.3	2663	4	US-09-538-092-1252	Sequence 1252, Ap
694	80.5	3.3	1861	2	US-08-790-912-4	Sequence 4861, A	767	79	3.3	85	4	US-09-430-221-12	Sequence 12, Appl
695	80.5	3.3	2108	4	US-09-538-092-87	Sequence 87, Appl	768	78.5	3.2	176	4	US-09-248-796A-14105	Sequence 14105, A
696	80	3.3	286	4	US-09-319-806-4	Sequence 4, Appl1	769	78.5	3.2	223	4	US-09-270-767-42765	Sequence 42765, A
697	80	3.3	310	4	US-09-98-520A-12	Sequence 12, Appl	770	78.5	3.2	302	4	US-09-252-991A-30761	Sequence 30761, A
698	80	3.3	377	4	US-09-252-991A-17627	Sequence 17627, A	771	78.5	3.2	329	4	US-09-252-991A-28843	Sequence 28843, A
699	80	3.3	379	4	US-09-489-039A-8383	Sequence 8383, Ap	772	78.5	3.2	331	3	US-09-134-001C-3526	Sequence 3526, Ap
700	80	3.3	397	4	US-09-248-796A-23498	Sequence 23498, A	773	78.5	3.2	336	4	US-09-138-185A-626	Sequence 626, App
701	80	3.3	478	4	US-09-902-540-15753	Sequence 15753, A	774	78.5	3.2	377	4	US-09-252-991A-19705	Sequence 19705, A
702	80	3.3	539	4	US-09-602-787A-196	Sequence 196, App	775	78.5	3.2	462	4	US-09-328-352-6483	Sequence 6483, Ap
703	80	3.3	544	4	US-09-489-039A-7235	Sequence 7235, Ap	776	78.5	3.2	466	3	US-08-740-223A-16	Sequence 16, Appl
704	80	3.3	550	3	US-09-120-365-1	Sequence 1, Appl1	777	78.5	3.2	496	4	US-09-709-188-16	Sequence 16, Appl
705	80	3.3	550	3	US-09-515-039-1	Sequence 1, Appl1	778	78.5	3.2	496	4	US-10-225-060-16	Sequence 16, Appl
706	80	3.3	601	4	US-09-902-540-14875	Sequence 14875, A	779	78.5	3.2	514	4	US-09-107-532A-4234	Sequence 4234, Ap
707	80	3.3	714	4	US-09-107-532A-5140	Sequence 5140, Ap	780	78.5	3.2	540	3	US-08-461-722-3	Sequence 3, Appl1
708	80	3.3	810	4	US-09-502-540-11337	Sequence 11337, A	781	78.5	3.2	540	3	US-08-336-251-3	Sequence 3, Appl1
709	80	3.3	821	4	US-09-377-465A-2	Sequence 2, Appl1	782	78.5	3.2	540	4	US-09-468-041-3	Sequence 3, Appl1
710	80	3.3	868	4	US-09-830-433A-73	Sequence 73, Appl	783	78.5	3.2	540	5	US-09-252-991A-28304	Sequence 28304, A
711	80	3.3	1030	3	US-09-091-117-2	Sequence 2, Appl1	784	78.5	3.2	542	4	US-09-252-991A-17653	Sequence 17653, A
712	80	3.3	1362	4	US-09-902-540-14577	Sequence 14577, A	785	78.5	3.2	551	4	US-09-248-796A-14711	Sequence 14711, A
713	80	3.3	1375	3	US-09-722-139-2	Sequence 2, Appl1	786	78.5	3.2	651	3	US-09-134-001C-4303	Sequence 4303, Ap
714	80	3.3	1375	3	US-09-721-832-2	Sequence 2, Appl1	787	78.5	3.2	738	4	US-09-538-092-818	Sequence 818, App
715	80	3.3	1375	3	US-09-721-832-2	Sequence 2, Appl1	788	78.5	3.2	747	3	US-09-724-864-36	Sequence 36, Appl
716	80	3.3	2482	4	US-09-252-991A-16967	Sequence 16967, A	789	78.5	3.2	795	4	US-09-134-000C-5968	Sequence 5968, Ap
717	80	3.3	3457	2	US-08-416-603-4	Sequence 4, Appl1	790	78.5	3.2	882	4	US-09-252-991A-17653	Sequence 17653, A
718	79.5	3.3	359	4	US-09-248-796A-17633	Sequence 17633, A	791	78.5	3.2	911	4	US-09-252-991A-19929	Sequence 19929, A
719	79.5	3.3	422	3	US-09-075-087-2	Sequence 2, Appl1	792	78.5	3.2	1068	3	US-09-315-694-7	Sequence 7, Appl1
720	79.5	3.3	432	3	US-09-472-971-1	Sequence 1, Appl1	793	78.5	3.2	1121	4	US-09-308-092-818	Sequence 818, App
721	79.5	3.3	442	4	US-09-134-000C-3694	Sequence 3694, Ap	794	78.5	3.2	1464	4	US-10-038-224-2	Sequence 2, Appl1
722	79.5	3.3	549	3	US-10-011-106-3	Sequence 3, Appl1	795	78.5	3.2	1525	3	US-09-396-651B-1	Sequence 1, Appl1
723	79.5	3.3	693	4	US-08-235-836C-72	Sequence 72, Appl	796	78	3.2	160	4	US-09-134-000C-4205	Sequence 4205, Ap
724	79.5	3.3	769	4	US-09-481-130A-18265	Sequence 18265, A	797	78	3.2	226	3	US-09-048-889-4	Sequence 4, Appl1
725	79.5	3.3	924	1	US-08-481-130A-28	Sequence 28, Appl	798	78	3.2	295	1	US-08-317-223-1	Sequence 1, Appl1
726	79.5	3.3	924	1	US-08-656-984A-28	Sequence 28, Appl	799	78	3.2	295	3	US-09-059-849A-1	Sequence 1, Appl1
727	79.5	3.3	924	1	US-08-485-604-28	Sequence 28, Appl	800	78	3.2	295	5	PCT-US93-12675-1	Sequence 1, Appl1
728	79.5	3.3	924	1	US-08-487-595-28	Sequence 28, Appl	801	78	3.2	323	3	US-09-120-365-61	Sequence 61, Appl
729	79.5	3.3	1244	5	PCT-US93-10500-2	Sequence 2, Appl1	802	78	3.2	323	3	US-09-515-039-61	Sequence 61, Appl
730	79.5	3.3	1288	1	US-07-727-814B-2	Sequence 2, Appl1	803	78	3.2	324	4	US-09-107-433-3719	Sequence 3719, Ap
731	79.5	3.3	1307	4	US-09-549-016-7561	Sequence 7561, Ap	804	78	3.2	368	4	US-09-107-433-4918	Sequence 4918, Ap
732	79.5	3.3	2777	4	US-09-943-681A-6124	Sequence 6124, Ap	805	78	3.2	382	4	US-09-248-796A-19559	Sequence 19559, A
733	79.5	3.3	3878	4	US-09-914-259-11	Sequence 11, Appl	806	78	3.2	404	4	US-09-949-016-10014	Sequence 10014, A
734	79.5	3.3	96	4	US-09-248-796A-17461	Sequence 17461, A	807	78	3.2	462	4	US-09-252-991A-27902	Sequence 27902, A
735	79	3.3	217	4	US-09-919-039-64	Sequence 64, Appl	808	78	3.2	497	4	US-09-902-540-12351	Sequence 12351, A
736	79	3.3	217	4	US-09-538-092-1029	Sequence 1029, Ap	809	78	3.2	508	4	US-09-802-540-11371	Sequence 11371, A
737	79	3.3	251	1	US-08-726-525-6	Sequence 6, Appl1	810	78	3.2	578	4	US-09-489-039A-8175	Sequence 8175, Ap
738	79	3.3	251	2	US-08-487-942-6	Sequence 6, Appl1	811	78	3.2	615	4	US-09-252-991A-27273	Sequence 27273, A
739	79	3.3	251	2	US-08-726-036A-6	Sequence 6, Appl1	812	78	3.2	631	4	US-09-252-991A-27902	Sequence 27902, A
740	79	3.3	251	2	US-08-726-036A-6	Sequence 6, Appl1	813	78	3.2	658	4	US-09-248-796A-20278	Sequence 20278, A
741	79	3.3	311	4	US-09-107-532A-4970	Sequence 4970, Ap	814	78	3.2	664	3	US-09-342-647-30	Sequence 30, Appl
742	79	3.3	340	3	US-09-120-365-60	Sequence 60, Appl	815	78	3.2	664	4	US-09-591-095-2	Sequence 2, Appl1
743	79	3.3	340	3	US-09-120-365-60	Sequence 60, Appl	816	78	3.2	923	4	US-09-949-016-8986	Sequence 8986, Ap
744	79	3.3	340	3	US-09-115-039-60	Sequence 60, Appl	817	78	3.2	967	3	US-08-816-346-56	Sequence 56, Appl
745	79	3.3	370	4	US-09-149-476-436	Sequence 436, App	818	78	3.2	967	3	US-09-335-411-56	Sequence 56, Appl
746	79	3.3	408	4	US-09-710-279-2286	Sequence 2286, Ap	819	78	3.2	968	3	US-08-816-346-56	Sequence 2, Appl1
747	79	3.3	436	4	US-09-248-796A-20561	Sequence 20561, A	820	78	3.2	968	3	US-09-335-411-56	Sequence 2, Appl1
748	79	3.3	485	4	US-09-489-039A-13826	Sequence 13826, A	821	78	3.2	968	3	US-09-335-411-56	Sequence 2, Appl1
749	79	3.3	485	4	US-09-543-681A-7006	Sequence 7006, Ap	822	78	3.2	976	3	US-09-104-324A-12	Sequence 4, Appl1
750	79	3.3	495	3	US-08-679-493A-164	Sequence 164, App	823	78	3.2	976	4	US-09-538-092-1339	Sequence 1339, Ap
751	79	3.3	624	1	US-09-252-991A-22637	Sequence 22637, A	824	78	3.2	1270	4	US-09-248-796A-15522	Sequence 15522, A
752	79	3.3	700	2	US-08-487-942-7	Sequence 7, Appl1	825	78	3.2	1285	3	US-09-308-375-2	Sequence 2, Appl1
753	79	3.3	700	2	US-08-487-942-7	Sequence 7, Appl1	826	78	3.2	2285	4	US-09-932-183A-2	Sequence 2, Appl1
754	79	3.3	700	2	US-08-726-036A-7	Sequence 23, Appl	827	77.5	3.2	208	4	US-09-107-532A-4287	Sequence 4287, Ap
755	79	3.3	700	3	US-09-422-869-23	Sequence 23, Appl	828	77.5	3.2	413	4	US-09-288-339-2	Sequence 2, Appl1
756	79	3.3	700	3	US-09-083-516-7	Sequence 7, Appl	829	77.5	3.2	463	1	US-07-748-292-9	Sequence 9, Appl
757	79	3.3	700	4	US-09-538-092-947	Sequence 947, App	830	77.5	3.2	463	3	US-08-867-611-31	Sequence 31, Appl

831	77.5	3.2	463	4	US-09-690-359-31	Sequence 31, Appl1	904	76.5	3.2	359	3	US-08-932-871B-1	Sequence 1, Appl1
832	77.5	3.2	463	5	PCT-US92-06965A-1	Sequence 1, Appl1	905	76.5	3.2	359	3	US-09-476-919-1	Sequence 1, Appl1
833	77.5	3.2	464	4	US-09-538-092-755	Sequence 755, App	906	76.5	3.2	359	3	US-08-780-311A-1	Sequence 1, Appl1
834	77.5	3.2	525	3	US-09-212-247C-11	Sequence 11, Appl	907	76.5	3.2	378	4	US-09-252-991A-23259	Sequence 23259, A
835	77.5	3.2	560	4	US-09-107-532A-4070	Sequence 4070, Ap	908	76.5	3.2	406	4	US-09-107-433-4169	Sequence 4169, Ap
836	77.5	3.2	566	4	US-09-328-352-4809	Sequence 4809, Ap	909	76.5	3.2	429	3	US-09-293-395-3	Sequence 3, Appl1
837	77.5	3.2	581	2	US-08-989-386-7	Sequence 7, Appl1	910	76.5	3.2	429	3	US-09-293-395-7	Sequence 7, Appl1
838	77.5	3.2	621	1	US-07-748-292-7	Sequence 7, Appl1	911	76.5	3.2	429	3	US-09-668-648-3	Sequence 3, Appl1
839	77.5	3.2	622	3	US-08-867-611-34	Sequence 34, Appl	912	76.5	3.2	429	3	US-09-668-648-7	Sequence 7, Appl1
840	77.5	3.2	622	3	US-09-650-359-34	Sequence 34, Appl	913	76.5	3.2	439	3	US-09-293-395-15	Sequence 15, Appl
841	77.5	3.2	622	5	PCT-US92-06965A-4	Sequence 4, Appl1	914	76.5	3.2	439	3	US-09-668-648-15	Sequence 15, Appl
842	77.5	3.2	637	2	US-08-426-125-10	Sequence 10, Appl	915	76.5	3.2	489	1	US-08-434-702-4	Sequence 4, Appl1
843	77.5	3.2	637	2	US-08-455-355-10	Sequence 10, Appl	916	76.5	3.2	489	1	US-09-302-540-9697	Sequence 9697, Ap
844	77.5	3.2	637	3	US-09-367-612-9	Sequence 9, Appl1	917	76.5	3.2	527	4	US-09-800-170-21	Sequence 21, Appl
845	77.5	3.2	728	3	US-08-867-611-35	Sequence 35, Appl	918	76.5	3.2	527	4	US-09-107-532A-4858	Sequence 4858, Ap
846	77.5	3.2	728	4	US-09-650-359-35	Sequence 35, Appl	919	76.5	3.2	553	4	US-09-302-540-16163	Sequence 16163, A
847	77.5	3.2	728	5	PCT-US92-06965A-5	Sequence 5, Appl1	920	76.5	3.2	554	4	US-09-198-452A-140	Sequence 140, App
848	77.5	3.2	829	4	US-09-438-185A-943	Sequence 943, App1	921	76.5	3.2	566	4	US-09-652-603-2	Sequence 2, Appl1
849	77.5	3.2	880	4	US-09-630-931A-19	Sequence 19, Appl	922	76.5	3.2	606	4	US-09-583-110-518	Sequence 518, Ap
850	77.5	3.2	944	4	US-09-437-568A-39	Sequence 39, Appl	923	76.5	3.2	606	4	US-09-107-433-4369	Sequence 4369, Ap
851	77.5	3.2	1166	3	US-09-352-159-31	Sequence 31, Appl	924	76.5	3.2	610	4	US-09-248-796A-18471	Sequence 18471, A
852	77.5	3.2	1166	3	US-09-352-168-31	Sequence 31, Appl	925	76.5	3.2	634	4	US-10-164-595-69	Sequence 69, Appl
853	77.5	3.2	1166	4	US-09-771-045B-31	Sequence 31, Appl	926	76.5	3.2	634	4	US-09-134-000C-4499	Sequence 4499, Ap
854	77.5	3.2	1196	4	US-09-770-564A-31	Sequence 31, Appl	927	76.5	3.2	639	4	US-09-302-540-11479	Sequence 11479, A
855	77.5	3.2	1279	4	US-09-710-279-3188	Sequence 318, Ap	928	76.5	3.2	718	4	US-09-252-991A-33109	Sequence 33109, A
856	77.5	3.2	1411	4	US-09-252-991A-23628	Sequence 23628, A	929	76.5	3.2	725	4	US-10-164-595A-30	Sequence 30, Appl
857	77.5	3.2	1457	4	US-09-713-273A-18	Sequence 18, Appl	930	76.5	3.2	742	4	US-09-500-123-12	Sequence 12, Appl
858	77.5	3.2	105	4	US-09-513-999C-5222	Sequence 5222, Ap	931	76.5	3.2	754	4	US-09-328-352-6501	Sequence 6501, Ap
859	77.5	3.2	187	4	US-09-248-796A-19329	Sequence 19329, A	932	76.5	3.2	848	4	US-09-556-877-192	Sequence 192, App
860	77.5	3.2	339	4	US-09-134-000C-4806	Sequence 4806, Ap	933	76.5	3.2	848	4	US-09-620-412C-132	Sequence 132, Appl
861	77.5	3.2	371	4	US-09-902-540-12556	Sequence 12556, A	934	76.5	3.2	848	4	US-09-598-419-192	Sequence 192, App
862	77.5	3.2	375	4	US-09-903-814A-2	Sequence 2, Appl1	935	76.5	3.2	871	4	US-09-500-123-7	Sequence 7, Appl1
863	77.5	3.2	375	4	US-10-723-061-2	Sequence 2, Appl1	936	76.5	3.2	1003	4	US-09-489-039A-12357	Sequence 12357, A
864	77.5	3.2	330	4	US-09-711-164-405	Sequence 405, App	937	76.5	3.2	1069	4	US-09-302-540-11566	Sequence 11566, A
865	77.5	3.2	406	4	US-09-248-796A-17915	Sequence 17915, A	938	76.5	3.2	1088	4	US-09-333-857-4	Sequence 4, US-09-333-857-4
866	77.5	3.2	409	1	US-09-723-546-14	Sequence 14, Appl	939	76.5	3.2	1220	3	US-08-930-996A-2	Sequence 2, Appl1
867	77.5	3.2	489	1	US-08-318-831-4	Sequence 4, Appl1	940	76.5	3.2	1530	4	US-09-620-412C-178	Sequence 178, App
868	77.5	3.2	495	3	US-09-134-001C-4273	Sequence 4273, Ap	941	76.5	3.2	1530	4	US-09-620-412C-178	Sequence 178, App
869	77.5	3.2	515	4	US-09-248-796A-19787	Sequence 19787, A	942	76.5	3.2	1530	4	US-09-598-419-178	Sequence 178, App
870	77.5	3.2	535	3	US-08-813-574-2	Sequence 2, Appl1	943	76.5	3.2	1315	1	US-08-323-170B-2	Sequence 2, Appl1
871	77.5	3.2	563	1	US-09-614-912-170	Sequence 170, App	944	76.5	3.1	3155	3	US-08-954-441-2	Sequence 2, Appl1
872	77.5	3.2	666	1	US-08-318-831-3	Sequence 3, Appl1	945	76.5	3.1	194	4	US-09-489-039A-7974	Sequence 7974, Ap
873	77.5	3.2	681	4	US-09-252-991A-28831	Sequence 28831, A	946	76.5	3.1	275	4	US-10-310-730-5	Sequence 5, Appl1
874	77.5	3.2	706	4	US-09-134-000C-5534	Sequence 5534, Ap	947	76.5	3.1	352	4	US-09-198-452A-582	Sequence 582, App
875	77.5	3.2	726	4	US-09-252-991A-26767	Sequence 26767, A	948	76.5	3.1	358	4	US-09-438-185A-346	Sequence 346, App
876	77.5	3.2	772	4	US-10-148-806-37	Sequence 37, Appl	949	76.5	3.1	367	4	US-09-252-991A-28059	Sequence 28059, A
877	77.5	3.2	790	4	US-09-949-016-7863	Sequence 7863, Ap	950	76.5	3.1	376	2	US-08-558-269-10	Sequence 10, Appl
878	77.5	3.2	814	1	US-08-318-831-2	Sequence 2, Appl1	951	76.5	3.1	376	3	US-09-410-882-10	Sequence 10, Appl
879	77.5	3.2	893	4	US-09-949-016-10267	Sequence 10267, A	952	76.5	3.1	401	4	US-09-252-991A-17372	Sequence 17372, A
880	77.5	3.2	893	4	US-09-949-016-10267	Sequence 10267, A	953	76.5	3.1	408	4	US-09-328-352-5768	Sequence 5768, Ap
881	77.5	3.2	983	3	US-09-412-554A-2	Sequence 2, Appl1	954	76.5	3.1	424	4	US-09-198-452A-45	Sequence 45, Appl
882	77.5	3.2	1043	3	US-09-538-092-935	Sequence 935, App	955	76.5	3.1	425	4	US-09-248-796A-17452	Sequence 17452, A
883	77.5	3.2	1410	3	US-09-335-409-3	Sequence 3, Appl1	956	76.5	3.1	451	4	US-09-538-092-706	Sequence 706, App
884	77.5	3.2	1410	3	US-09-568-102-3	Sequence 3, Appl1	957	76.5	3.1	533	4	US-09-543-681A-4664	Sequence 4664, Ap
885	77.5	3.2	1410	3	US-09-567-969-3	Sequence 3, Appl1	958	76.5	3.1	595	4	US-09-949-016-7811	Sequence 7811, Ap
886	77.5	3.2	1410	3	US-09-568-480-3	Sequence 3, Appl1	959	76.5	3.1	620	4	US-09-673-198-1	Sequence 1, Appl1
887	77.5	3.2	1410	3	US-09-568-486-3	Sequence 3, Appl1	960	76.5	3.1	631	4	US-09-252-991A-26007	Sequence 26007, A
888	77.5	3.2	1410	3	US-09-568-472-3	Sequence 3, Appl1	961	76.5	3.1	656	4	US-09-489-039A-82312	Sequence 8212, Ap
889	77.5	3.2	1410	3	US-09-567-899-3	Sequence 3, Appl1	962	76.5	3.1	674	3	US-08-961-083A-200	Sequence 200, App
890	77.5	3.2	1425	4	US-09-248-796A-18447	Sequence 18447, A	963	76.5	3.1	674	4	US-09-536-784A-200	Sequence 200, App
891	77.5	3.2	1966	2	US-08-804-227C-9	Sequence 9, Appl1	964	76.5	3.1	666	4	US-09-252-991A-28636	Sequence 28636, A
892	77.5	3.2	1996	2	US-08-804-198-3	Sequence 3, Appl1	965	76.5	3.1	836	4	US-09-858-525B-10	Sequence 10, Appl
893	76.5	3.2	61	4	US-09-270-767-59015	Sequence 59015, A	966	76.5	3.1	871	3	US-09-558-525B-2	Sequence 2, Appl1
894	76.5	3.2	288	4	US-09-489-039A-8919	Sequence 8919, Ap	967	76.5	3.1	873	3	US-09-558-525B-2	Sequence 2, Appl1
895	76.5	3.2	317	2	US-09-066-075-2	Sequence 2, Appl1	968	76.5	3.1	873	3	US-09-546-238-2	Sequence 2, Appl1
896	76.5	3.2	317	3	US-08-518-615A-2	Sequence 2, Appl1	969	76.5	3.1	1149	4	US-09-543-681A-7306	Sequence 7306, Ap
897	76.5	3.2	317	3	US-08-951-889-2	Sequence 2, Appl1	970	76.5	3.1	1211	4	US-09-328-352-7957	Sequence 7957, Ap
898	76.5	3.2	317	3	US-09-472-857-2	Sequence 2, Appl1	971	76.5	3.1	1257	4	US-09-107-532A-4552	Sequence 4552, Ap
899	76.5	3.2	332	4	US-09-498-520A-10	Sequence 10, Appl	972	76.5	3.1	1783	4	US-09-362-336A-2	Sequence 2, Appl1
900	76.5	3.2	332	4	US-09-134-000C-4988	Sequence 4988, Ap	973	76.5	3.1	1804	4	US-09-362-336A-4	Sequence 4, Appl1
901	76.5	3.2	358	4	US-09-248-796A-18232	Sequence 18232, A	974	76.5	3.1	2375	4	US-09-538-092-1131	Sequence 1131, Ap
902	76.5	3.2	359	2	US-08-483-926A-8	Sequence 8, Appl1	975	75.5	3.1	189	4	US-09-370-767-47683	Sequence 47683, A
903	76.5	3.2	359	2	US-08-737-045-11	Sequence 11, Appl	976	75.5	3.1	199	4	US-09-802-540-11406	Sequence 11406, A

977	75.5	3.1	238	4	US-09-583-110-5109	Sequence 5109, Ap	1050	75	3.1	2517	4	US-09-302-540-15380	Sequence 15380, A
978	75.5	3.1	239	4	US-09-107-433-3599	Sequence 3599, Ap	1051	75	3.1	2887	3	US-08-462-467B-2	Sequence 2, Appl1
979	75.5	3.1	306	4	US-09-302-540-11052	Sequence 11052, A	1052	75	3.1	2887	3	US-08-462-467B-8	Sequence 8, Appl1
980	75.5	3.1	324	4	US-09-498-520A-2	Sequence 2, Appl1	1053	75	3.1	3072	3	US-09-413-814-93	Sequence 93, Appl1
981	75.5	3.1	324	4	US-09-968-129-2	Sequence 2, Appl1	1054	75	3.1	3079	3	US-09-413-814-80	Sequence 80, Appl1
982	75.5	3.1	328	4	US-09-252-991A-30302	Sequence 30302, A	1055	75	3.1	3421	4	US-09-452-638-53	Sequence 53, Appl1
983	75.5	3.1	376	4	US-09-98-520A-32	Sequence 32, Appl1	1056	74.5	3.1	125	4	US-09-513-999C-5278	Sequence 5278, Ap
984	75.5	3.1	367	4	US-09-543-681A-7199	Sequence 7199, Ap	1057	74.5	3.1	184	4	US-09-107-532A-5591	Sequence 5591, Ap
985	75.5	3.1	453	4	US-09-252-991A-17641	Sequence 17641, A	1058	74.5	3.1	203	4	US-09-270-767-57598	Sequence 57598, A
986	75.5	3.1	505	4	US-09-270-767-43185	Sequence 43185, A	1059	74.5	3.1	233	4	US-09-328-352-6059	Sequence 6059, Ap
987	75.5	3.1	509	4	US-09-543-681A-5944	Sequence 5944, Ap	1060	74.5	3.1	292	4	US-09-248-796A-20567	Sequence 20567, A
988	75.5	3.1	535	4	US-09-312-762A-10	Sequence 10, Appl1	1061	74.5	3.1	332	4	US-09-602-787A-112	Sequence 112, App
989	75.5	3.1	535	4	US-09-949-016-6879	Sequence 6879, Ap	1062	74.5	3.1	336	4	US-09-107-532A-7113	Sequence 7113, Ap
990	75.5	3.1	570	4	US-09-949-016-7440	Sequence 7440, Ap	1063	74.5	3.1	339	4	US-09-107-532A-5819	Sequence 5819, Ap
991	75.5	3.1	609	4	US-09-248-796A-19292	Sequence 19292, A	1064	74.5	3.1	338	4	US-09-252-991A-26841	Sequence 26841, A
992	75.5	3.1	666	4	US-08-441-139-16	Sequence 16, Appl1	1065	74.5	3.1	340	4	US-09-128-352-5334	Sequence 5334, Ap
993	75.5	3.1	712	4	US-09-543-681A-8147	Sequence 8147, Ap	1066	74.5	3.1	343	4	US-09-489-039A-9178	Sequence 9178, Ap
994	75.5	3.1	742	4	US-09-107-532A-4996	Sequence 4996, Ap	1067	74.5	3.1	345	3	US-09-120-365-73	Sequence 73, Appl1
995	75.5	3.1	749	4	US-09-562-737-96	Sequence 96, Appl1	1068	74.5	3.1	345	3	US-09-515-039-73	Sequence 73, Appl1
996	75.5	3.1	766	4	US-09-302-540-10602	Sequence 10602, A	1069	74.5	3.1	345	3	US-08-827-171B-7	Sequence 7, Appl1
997	75.5	3.1	773	3	US-08-564-264-1	Sequence 1, Appl1	1070	74.5	3.1	345	4	US-09-598-062-7	Sequence 6, Appl1
998	75.5	3.1	803	2	US-08-907-166-4	Sequence 4, Appl1	1071	74.5	3.1	353	3	US-08-986-485-6	Sequence 19518, A
999	75.5	3.1	803	4	US-09-391-340-4	Sequence 4, Appl1	1072	74.5	3.1	370	4	US-09-252-991A-19518	Sequence 19518, A
1000	75.5	3.1	812	4	US-09-489-039A-12075	Sequence 12075, A	1073	74.5	3.1	378	4	US-09-583-110-3941	Sequence 3941, Ap
1001	75.5	3.1	924	4	US-09-583-110-3216	Sequence 3216, Ap	1074	74.5	3.1	378	4	US-09-107-433-5197	Sequence 5197, Ap
1002	75.5	3.1	928	4	US-09-107-433-2917	Sequence 2917, Ap	1075	74.5	3.1	404	4	US-09-107-532A-7113	Sequence 6741, Ap
1003	75.5	3.1	1165	4	US-09-887-052-2	Sequence 2, Appl1	1076	74.5	3.1	426	4	US-09-252-991A-31959	Sequence 31959, A
1004	75.5	3.1	1165	4	US-09-887-052-4	Sequence 4, Appl1	1077	74.5	3.1	429	4	US-09-470-767-43353	Sequence 43353, A
1005	75.5	3.1	1165	4	US-09-887-052-6	Sequence 6, Appl1	1078	74.5	3.1	437	4	US-09-543-681A-6277	Sequence 6277, Ap
1006	75.5	3.1	1168	4	US-09-762-311-5	Sequence 5, Appl1	1079	74.5	3.1	438	4	US-09-352-991A-16710	Sequence 16710, A
1007	75.5	3.1	1197	4	US-09-618-425-2	Sequence 2, Appl1	1080	74.5	3.1	467	3	US-08-867-611-24	Sequence 24, Appl1
1008	75.5	3.1	1395	4	US-09-949-016-7109	Sequence 7109, Ap	1081	74.5	3.1	467	4	US-09-690-359-24	Sequence 24, Appl1
1009	75.5	3.1	1778	4	US-09-252-991A-18159	Sequence 18159, A	1082	74.5	3.1	467	5	PCT-US92-06965A-29	Sequence 29, Appl1
1010	75.5	3.1	1998	4	US-09-949-016-6417	Sequence 6417, Ap	1083	74.5	3.1	484	4	US-09-107-532A-3830	Sequence 3830, Ap
1011	75.5	3.1	3696	3	US-09-134-001C-5080	Sequence 5080, Ap	1084	74.5	3.1	488	2	US-08-797-226-2	Sequence 2, Appl1
1012	75	3.1	164	4	US-09-252-991A-22887	Sequence 22887, A	1085	74.5	3.1	498	4	US-09-489-039A-13707	Sequence 13707, A
1013	75	3.1	179	4	US-09-134-000C-6637	Sequence 6637, Ap	1086	74.5	3.1	505	4	US-09-198-445A-1117	Sequence 1117, Ap
1014	75	3.1	229	4	US-09-302-540-9723	Sequence 9723, Ap	1087	74.5	3.1	526	4	US-09-438-185A-1042	Sequence 1042, Ap
1015	75	3.1	248	4	US-09-134-000C-4356	Sequence 4356, Ap	1088	74.5	3.1	534	4	US-09-312-762A-4	Sequence 4, Appl1
1016	75	3.1	253	4	US-09-252-991A-26495	Sequence 26495, A	1089	74.5	3.1	557	4	US-09-540-236-2206	Sequence 2206, Ap
1017	75	3.1	257	4	US-09-248-796A-17775	Sequence 17775, A	1090	74.5	3.1	558	4	US-09-309-572-5	Sequence 5, Appl1
1018	75	3.1	284	2	US-08-538-960-2	Sequence 2, Appl1	1091	74.5	3.1	558	4	US-09-118-096-5	Sequence 5, Appl1
1019	75	3.1	313	4	US-09-583-110-4768	Sequence 4768, Ap	1092	74.5	3.1	577	4	US-09-252-991A-26876	Sequence 26876, A
1020	75	3.1	315	1	US-08-257-073-7	Sequence 7, Appl1	1093	74.5	3.1	578	4	US-08-635-552A-2	Sequence 2, Appl1
1021	75	3.1	320	4	US-09-902-540-12450	Sequence 12450, A	1094	74.5	3.1	589	4	US-09-949-016-11530	Sequence 11530, A
1022	75	3.1	385	4	US-09-902-540-10348	Sequence 10348, A	1095	74.5	3.1	600	6	5240706-1	Patent No. 5240706
1023	75	3.1	397	4	US-09-252-991A-20713	Sequence 20713, A	1096	74.5	3.1	600	6	5240706-1	Patent No. 5240706
1024	75	3.1	397	4	US-09-502-540-12231	Sequence 12231, A	1097	74.5	3.1	603	1	US-08-190-802A-50	Sequence 50, Appl1
1025	75	3.1	398	4	US-09-543-681A-7639	Sequence 7639, Ap	1098	74.5	3.1	603	3	US-08-477-346-50	Sequence 50, Appl1
1026	75	3.1	476	4	US-09-291-299A-3	Sequence 3, Appl1	1099	74.5	3.1	603	3	US-08-473-089-50	Sequence 50, Appl1
1027	75	3.1	555	3	US-09-813-872-4	Sequence 4, Appl1	1100	74.5	3.1	603	4	US-08-487-072A-50	Sequence 50, Appl1
1028	75	3.1	615	4	US-09-328-352-4474	Sequence 4474, Ap	1101	74.5	3.1	610	2	US-08-974-565C-9	Sequence 9, Appl1
1029	75	3.1	663	4	US-09-949-016-7198	Sequence 7198, Ap	1102	74.5	3.1	610	2	US-08-642-521B-7	Sequence 7, Appl1
1030	75	3.1	717	4	US-09-252-991A-25715	Sequence 25715, A	1103	74.5	3.1	610	3	US-09-235-748-9	Sequence 9, Appl1
1031	75	3.1	789	4	US-09-949-016-7237	Sequence 7237, Ap	1104	74.5	3.1	654	4	US-09-489-039A-7948	Sequence 7948, Ap
1032	75	3.1	817	4	US-09-248-796A-17089	Sequence 17089, A	1105	74.5	3.1	655	4	US-09-228-986-70	Sequence 70, Appl1
1033	75	3.1	829	4	US-09-514-599-6	Sequence 6, Appl1	1106	74.5	3.1	655	4	US-10-101-464A-70	Sequence 70, Appl1
1034	75	3.1	829	4	US-09-996-024-6	Sequence 6, Appl1	1107	74.5	3.1	661	4	US-09-252-991A-26533	Sequence 26533, A
1035	75	3.1	862	3	US-09-346-237-1	Sequence 1, Appl1	1108	74.5	3.1	681	4	US-09-248-796A-20472	Sequence 20472, A
1036	75	3.1	862	4	US-09-328-352-6286	Sequence 6286, Ap	1109	74.5	3.1	693	4	US-09-502-540-15393	Sequence 15393, A
1037	75	3.1	873	4	US-09-489-039A-11755	Sequence 11755, A	1110	74.5	3.1	703	4	US-09-489-039A-8335	Sequence 8335, Ap
1038	75	3.1	883	4	US-09-630-929-3	Sequence 3, Appl1	1111	74.5	3.1	728	3	US-09-134-001C-4266	Sequence 4266, Ap
1039	75	3.1	898	4	US-09-489-039A-10322	Sequence 10322, A	1112	74.5	3.1	743	4	US-09-489-039A-11310	Sequence 11310, A
1040	75	3.1	919	4	US-09-270-767-44725	Sequence 44725, A	1113	74.5	3.1	760	4	US-09-449-016-10675	Sequence 10675, A
1041	75	3.1	951	3	US-08-816-346-58	Sequence 58, Appl1	1114	74.5	3.1	796	2	US-08-817-900-2	Sequence 2, Appl1
1042	75	3.1	951	3	US-09-335-411-58	Sequence 58, Appl1	1115	74.5	3.1	796	3	US-09-336-645-2	Sequence 2, Appl1
1043	75	3.1	952	2	US-08-788-674-5	Sequence 4, Appl1	1116	74.5	3.1	815	1	US-08-122-520C-9	Sequence 9, Appl1
1044	75	3.1	952	3	US-08-816-346-4	Sequence 4, Appl1	1117	74.5	3.1	892	4	US-09-543-681A-8314	Sequence 8314, Ap
1045	75	3.1	952	3	US-09-335-411-4	Sequence 4, Appl1	1118	74.5	3.1	906	1	US-08-687-379-2	Sequence 2, Appl1
1046	75	3.1	1351	4	US-09-489-039A-11032	Sequence 11032, A	1119	74.5	3.1	906	1	US-08-687-379-2	Sequence 2, Appl1
1047	75	3.1	1401	4	US-09-750-590A-2	Sequence 2, Appl1	1120	74.5	3.1	912	4	US-09-328-352-5333	Sequence 5323, Ap
1048	75	3.1	1618	3	US-08-462-467B-4	Sequence 4, Appl1	1121	74.5	3.1	1025	4	US-09-711-164-443	Sequence 443, App
1049	75	3.1	1881	3	US-09-233-086-3	Sequence 3, Appl1	1122	74.5	3.1	1025	4	US-09-492-709A-283	Sequence 283, App

1123	74.5	3.1	1032	4	US-09-949-016-10553	Sequence 10553, A	1196	74	3.1	1087	1	US-08-264-002-5	Sequence 5, Appl1
1124	74.5	3.1	1055	3	US-09-031-563-27	Sequence 27, Appl1	1197	74	3.1	1218	4	US-09-198-452A-98	Sequence 96, Appl1
1125	74.5	3.1	1055	4	US-09-392-277-27	Sequence 27, Appl1	1198	74	3.1	1279	4	US-09-538-092-976	Sequence 956, App
1126	74.5	3.1	1055	4	US-09-258-000-27	Sequence 27, Appl1	1199	74	3.1	1290	4	US-09-538-092-956	Sequence 956, App
1127	74.5	3.1	1242	4	US-09-583-110-5051	Sequence 5051, Ap	1200	74	3.1	1312	4	US-09-949-016-10141	Sequence 10141, A
1128	74.5	3.1	1243	4	US-09-107-433-3942	Sequence 3942, Ap	1201	74	3.1	1410	4	US-09-438-185A-84	Sequence 84, Appl1
1129	74.5	3.1	1299	5	PCT-US95-08354A-2	Sequence 2, Appl1	1202	74	3.1	1666	4	US-09-902-540-15792	Sequence 15792, A
1130	74.5	3.1	1315	3	US-09-031-563-2	Sequence 2, Appl1	1203	74	3.1	1938	4	US-09-514-302-2	Sequence 2, Appl1
1131	74.5	3.1	1315	3	US-09-031-563-25	Sequence 25, Appl1	1204	74	3.1	1938	4	US-10-014-436-2	Sequence 2, Appl1
1132	74.5	3.1	1315	3	US-09-293-505-10	Sequence 10, Appl1	1205	74	3.1	3472	4	US-09-902-540-9732	Sequence 9732, Ap
1133	74.5	3.1	1315	3	US-09-392-277-2	Sequence 2, Appl1	1206	74	3.1	3472	4	US-09-408-020-4	Sequence 4, Appl1
1134	74.5	3.1	1315	4	US-09-392-277-25	Sequence 25, Appl1	1207	74	3.1	109	3	US-09-399-913-34	Sequence 34, Appl1
1135	74.5	3.1	1315	4	US-09-258-000-2	Sequence 2, Appl1	1208	74.5	3.0	109	3	US-09-298-731-34	Sequence 34, Appl1
1136	74.5	3.1	1315	4	US-09-050-939A-10	Sequence 25, Appl1	1209	73.5	3.0	109	4	US-09-350-514-34	Sequence 34, Appl1
1137	74.5	3.1	1315	4	US-08-496-944-2	Sequence 10, Appl1	1210	73.5	3.0	222	1	US-07-688-352C-46	Sequence 46, Appl1
1138	74.5	3.1	2763	3	US-08-496-944-2	Sequence 2, Appl1	1211	73.5	3.0	222	5	PCT-US91-02714-43	Sequence 46, Appl1
1139	74.5	3.1	3169	3	US-09-453-702B-257	Sequence 257, App	1212	73.5	3.0	222	5	PCT-US91-02714-43	Sequence 53, Appl1
1140	74.5	3.1	3443	2	US-08-416-603-2	Sequence 2, Appl1	1213	73.5	3.0	223	2	US-08-190-199A-63	Sequence 63, Appl1
1141	74	3.1	126	4	US-09-205-258-1076	Sequence 1076, Ap	1214	73.5	3.0	240	2	US-08-956-047-25	Sequence 25, Appl1
1142	74	3.1	207	4	US-09-248-796A-15790	Sequence 15790, A	1215	73.5	3.0	253	2	US-08-474-379C-46	Sequence 46, Appl1
1143	74	3.1	217	4	US-09-248-796A-21994	Sequence 21994, A	1216	73.5	3.0	253	3	US-09-146-249A-46	Sequence 46, Appl1
1144	74	3.1	251	4	US-09-440-967-2	Sequence 2, Appl1	1217	73.5	3.0	253	3	US-08-206-188B-46	Sequence 46, Appl1
1145	74	3.1	254	1	US-08-425-336-107	Sequence 107, App	1218	73.5	3.0	280	3	US-08-652-877-6	Sequence 6, Appl1
1146	74	3.1	251	1	US-08-488-113B-107	Sequence 107, App	1219	73.5	3.0	301	3	US-08-476-515A-6	Sequence 6, Appl1
1147	74	3.1	251	1	US-08-477-484B-107	Sequence 107, App	1220	73.5	3.0	301	3	US-09-188-930-145	Sequence 145, App
1148	74	3.1	251	2	US-08-646-360-107	Sequence 107, App	1221	73.5	3.0	301	3	US-09-188-930-149	Sequence 149, App
1149	74	3.1	251	2	US-08-839-765-107	Sequence 107, App	1222	73.5	3.0	301	4	US-09-312-283C-145	Sequence 145, App
1150	74	3.1	251	3	US-09-136-389-107	Sequence 107, App	1223	73.5	3.0	301	4	US-09-312-283C-149	Sequence 145, App
1151	74	3.1	251	3	US-09-610-838-107	Sequence 107, App	1224	73.5	3.0	314	4	US-09-902-540-14628	Sequence 14628, A
1152	74	3.1	251	3	US-09-711-485-107	Sequence 107, App	1225	73.5	3.0	331	4	US-10-010-580-2	Sequence 2, Appl1
1153	74	3.1	285	4	US-09-328-352-6464	Sequence 6464, Ap	1226	73.5	3.0	378	4	US-09-325-932A-158	Sequence 158, App
1154	74	3.1	302	4	US-09-328-352-5520	Sequence 5520, Ap	1227	73.5	3.0	383	4	US-09-902-540-1640	Sequence 1640, A
1155	74	3.1	313	4	US-09-648-004-14	Sequence 14, Appl1	1228	73.5	3.0	403	4	US-08-311-731A-104	Sequence 104, App
1156	74	3.1	313	4	US-10-272-419-14	Sequence 14, Appl1	1229	73.5	3.0	406	4	US-08-311-731A-12	Sequence 12, Appl1
1157	74	3.1	317	4	US-08-461-607-7	Sequence 9, Appl1	1230	73.5	3.0	410	4	US-09-755-630B-290	Sequence 290, App
1158	74	3.1	324	3	US-08-461-607-7	Sequence 7, Appl1	1231	73.5	3.0	410	4	US-09-755-274-10	Sequence 10, Appl1
1159	74	3.1	324	3	US-09-363-600-7	Sequence 7, Appl1	1232	73.5	3.0	422	4	US-09-489-039A-10842	Sequence 10842, A
1160	74	3.1	326	3	US-09-134-001C-4721	Sequence 4721, Ap	1233	73.5	3.0	443	4	US-09-328-352-7725	Sequence 7725, Ap
1161	74	3.1	326	4	US-09-583-110-0330	Sequence 4330, Ap	1234	73.5	3.0	444	3	US-09-188-930-296	Sequence 296, App
1162	74	3.1	330	4	US-09-724-797-28	Sequence 28, Appl1	1235	73.5	3.0	444	4	US-09-312-283C-296	Sequence 296, App
1163	74	3.1	335	4	US-09-222-938A-4	Sequence 4, Appl1	1236	73.5	3.0	444	4	US-09-312-283C-406	Sequence 406, App
1164	74	3.1	337	4	US-09-328-352-6980	Sequence 6980, Ap	1237	73.5	3.0	453	4	US-09-902-540-15539	Sequence 15539, A
1165	74	3.1	339	3	US-08-444-818-156	Sequence 156, App	1238	73.5	3.0	471	1	US-08-257-341-9	Sequence 9, Appl1
1166	74	3.1	345	4	US-09-543-681A-7546	Sequence 7546, Ap	1239	73.5	3.0	481	1	US-08-286-856C-2	Sequence 2, Appl1
1167	74	3.1	375	4	US-09-248-796A-19016	Sequence 19016, A	1240	73.5	3.0	481	1	US-08-472-831-2	Sequence 2, Appl1
1168	74	3.1	376	4	US-09-902-540-9959	Sequence 9959, Ap	1241	73.5	3.0	484	4	US-09-489-039A-7690	Sequence 7690, Ap
1169	74	3.1	418	4	US-09-688-188B-99	Sequence 99, Appl1	1242	73.5	3.0	484	4	US-09-820-007-4	Sequence 4, Appl1
1170	74	3.1	418	4	US-09-291-417D-99	Sequence 99, Appl1	1243	73.5	3.0	499	4	US-09-949-016-8268	Sequence 8268, Ap
1171	74	3.1	430	4	US-09-540-236-3267	Sequence 3267, Ap	1244	73.5	3.0	501	2	US-08-577-492-40	Sequence 40, Appl1
1172	74	3.1	438	4	US-09-328-352-6511	Sequence 6511, Ap	1245	73.5	3.0	501	3	US-09-079-630-40	Sequence 40, Appl1
1173	74	3.1	456	4	US-09-583-110-9651	Sequence 3651, Ap	1246	73.5	3.0	505	4	US-09-252-991A-29343	Sequence 29343, A
1174	74	3.1	456	4	US-09-107-433-5001	Sequence 5001, Ap	1247	73.5	3.0	506	1	US-08-286-856C-3	Sequence 3, Appl1
1175	74	3.1	475	4	US-09-328-352-5706	Sequence 5706, Ap	1248	73.5	3.0	506	1	US-08-472-831-3	Sequence 3, Appl1
1176	74	3.1	475	4	US-09-711-164-403	Sequence 403, App	1249	73.5	3.0	519	4	US-09-820-007-2	Sequence 2, Appl1
1177	74	3.1	485	4	US-09-639-245-8	Sequence 8, Appl1	1250	73.5	3.0	522	4	US-09-252-991A-16994	Sequence 16994, A
1178	74	3.1	495	4	US-09-107-532A-4081	Sequence 4081, Ap	1251	73.5	3.0	534	4	US-09-312-762A-5	Sequence 5, Appl1
1179	74	3.1	502	4	US-09-489-039A-10638	Sequence 10638, A	1252	73.5	3.0	536	4	US-09-930-218-2	Sequence 2, Appl1
1180	74	3.1	506	4	US-09-252-991A-32150	Sequence 32150, A	1253	73.5	3.0	566	4	US-09-252-991A-17705	Sequence 17705, A
1181	74	3.1	542	4	US-09-252-991A-18457	Sequence 18457, A	1254	73.5	3.0	606	2	US-08-577-492-32	Sequence 32, Appl1
1182	74	3.1	566	4	US-09-328-352-7811	Sequence 7811, Ap	1255	73.5	3.0	606	3	US-09-079-630-32	Sequence 32, Appl1
1183	74	3.1	580	4	US-09-252-991A-27245	Sequence 27245, A	1256	73.5	3.0	670	4	US-09-134-000C-4606	Sequence 4606, Ap
1184	74	3.1	606	4	US-09-603-208A-56	Sequence 56, Appl1	1257	73.5	3.0	700	4	US-09-502-540-11872	Sequence 11872, A
1185	74	3.1	641	4	US-09-919-039-146	Sequence 146, App	1258	73.5	3.0	727	4	US-09-585-858-32	Sequence 32, Appl1
1186	74	3.1	648	4	US-09-489-039A-12514	Sequence 12514, A	1259	73.5	3.0	727	4	US-10-270-878-32	Sequence 32, Appl1
1187	74	3.1	659	3	US-09-134-001C-5537	Sequence 5537, Ap	1260	73.5	3.0	773	4	US-09-913-301-5	Sequence 5, Appl1
1188	74	3.1	676	4	US-09-107-532A-5627	Sequence 5627, Ap	1261	73.5	3.0	775	1	US-07-966-278-1	Sequence 1, Appl1
1189	74	3.1	710	4	US-09-902-540-16023	Sequence 16023, A	1262	73.5	3.0	775	1	US-08-424-921-1	Sequence 1, Appl1
1190	74	3.1	754	4	US-09-902-540-14485	Sequence 14485, A	1263	73.5	3.0	775	2	US-08-556-355A-1	Sequence 1, Appl1
1191	74	3.1	879	4	US-09-252-991A-19784	Sequence 19784, A	1264	73.5	3.0	775	2	US-07-803-627B-1	Sequence 1, Appl1
1192	74	3.1	893	3	US-09-514-302-4	Sequence 4, Appl1	1265	73.5	3.0	775	4	US-09-244-889A-1	Sequence 1, Appl1
1193	74	3.1	893	3	US-10-014-436-4	Sequence 4, Appl1	1266	73.5	3.0	804	2	US-08-688-649-37	Sequence 37, Appl1
1194	74	3.1	962	3	US-09-134-001C-4497	Sequence 4497, Ap	1267	73.5	3.0	804	4	US-09-913-301-2	Sequence 2, Appl1
1195	74	3.1	1040	4	US-09-489-039A-13619	Sequence 13619, A	1268	73.5	3.0	844	4	US-09-640-958-8	Sequence 8, Appl1

1269	73.5	3.0	904	4	US-09-328-352-4656	Sequence 4656, Ap	1342	73	3.0	676	4	US-09-198-452A-836	Sequence 836, App
1270	73.5	3.0	906	1	US-08-254-573-2	Sequence 2, Appl1	1343	73	3.0	678	4	US-07-583-110-3885	Sequence 3885, Ap
1271	73.5	3.0	906	1	US-08-172-332-1	Sequence 1, Appl1	1344	73	3.0	700	1	US-07-720-589-2	Sequence 2, Appl1
1272	73.5	3.0	906	4	US-08-216-326-2	Sequence 2, Appl1	1345	73	3.0	700	2	US-08-785-190-2	Sequence 2, Appl1
1273	73.5	3.0	923	3	US-09-397-885-1	Sequence 1, Appl1	1346	73	3.0	700	5	PCT-US92-05539-2	Sequence 2, Appl1
1274	73.5	3.0	923	4	US-09-369-362-1	Sequence 1, Appl1	1347	73	3.0	710	4	US-09-134-000C-6451	Sequence 6451, Ap
1275	73.5	3.0	1011	4	US-09-252-991A-32419	Sequence 32419, A	1348	73	3.0	719	4	US-09-438-185A-788	Sequence 788, App
1276	73.5	3.0	1078	4	US-09-248-796A-20284	Sequence 20284, A	1349	73	3.0	721	4	US-09-438-185A-788	Sequence 17831, A
1277	73.5	3.0	1145	4	US-09-438-185A-191	Sequence 191, App	1350	73	3.0	723	4	US-09-489-039A-11108	Sequence 11108, A
1278	73.5	3.0	3724	2	US-08-804-227C-10	Sequence 10, Appl	1351	73	3.0	724	4	US-09-438-185A-135	Sequence 125, App
1279	73.5	3.0	3724	2	US-08-804-198-A	Sequence 4, Appl1	1352	73	3.0	753	2	US-09-328-352-4406	Sequence 4406, Ap
1280	73.5	3.0	5588	3	US-09-036-987A-6	Sequence 6, Appl1	1353	73	3.0	793	2	US-08-468-558-5	Sequence 5, Appl1
1281	73.5	3.0	5588	3	US-09-370-700-6	Sequence 6, Appl1	1354	73	3.0	793	3	US-08-676-444-5	Sequence 5, Appl1
1282	73.5	3.0	5588	4	US-09-603-207-6	Sequence 6, Appl1	1355	73	3.0	844	4	US-09-591-258-19	Sequence 19, Appl
1283	73	3.0	225	4	US-09-328-352-4179	Sequence 4179, Ap	1356	73	3.0	915	4	US-09-817-514A-6	Sequence 6, Appl1
1284	73	3.0	226	4	US-09-248-796A-16182	Sequence 16182, A	1357	73	3.0	956	1	US-08-185-232A-2	Sequence 2, Appl1
1285	73	3.0	227	3	US-09-181-183-32	Sequence 32, Appl	1358	73	3.0	956	1	US-08-416-523-2	Sequence 2, Appl1
1286	73	3.0	227	3	US-09-280-040-32	Sequence 32, Appl	1359	73	3.0	966	3	US-08-789-478-2	Sequence 2, Appl1
1287	73	3.0	227	3	US-09-277-700-32	Sequence 32, Appl	1360	73	3.0	989	4	US-09-079-030-218	Sequence 218, App
1288	73	3.0	227	4	US-09-874-585D-32	Sequence 32, Appl	1361	73	3.0	1074	4	US-09-302-540-10427	Sequence 10427, A
1289	73	3.0	227	4	US-09-874-585D-32	Sequence 32, Appl	1362	73	3.0	1101	2	US-08-469-537A-96	Sequence 96, Appl
1290	73	3.0	258	4	US-09-902-540-13979	Sequence 56, Appl	1363	73	3.0	1279	4	US-09-489-039A-13602	Sequence 13602, A
1291	73	3.0	256	4	US-09-602-787A-174	Sequence 174, App	1364	73	3.0	1561	4	US-09-543-681A-6604	Sequence 6604, Ap
1292	73	3.0	324	4	US-09-148-545-181	Sequence 181, App	1365	73	3.0	1785	3	US-09-341-587-3	Sequence 3, Appl1
1293	73	3.0	324	4	US-09-252-991A-30665	Sequence 30665, A	1366	73	3.0	2362	3	US-09-949-016-8985	Sequence 8985, Ap
1294	73	3.0	342	4	US-09-489-039A-7507	Sequence 7507, Ap	1367	73	3.0	4544	4	US-08-469-486-52	Sequence 52, Appl
1295	73	3.0	345	4	US-09-543-681A-6954	Sequence 6954, Ap	1368	73	3.0	4544	2	US-08-469-658-52	Sequence 52, Appl
1296	73	3.0	348	4	US-09-252-991A-26643	Sequence 26643, A	1369	73	3.0	4866	4	US-09-424-783-2	Sequence 2, Appl1
1297	73	3.0	356	4	US-09-328-352-6258	Sequence 6258, Ap	1370	73	3.0	54	4	US-09-513-999C-6743	Sequence 6743, Ap
1298	73	3.0	374	4	US-09-252-991A-18114	Sequence 18114, A	1371	72.5	3.0	65	4	US-09-513-999C-5364	Sequence 5364, Ap
1299	73	3.0	374	4	US-09-252-991A-18114	Sequence 22367, A	1372	72.5	3.0	206	4	US-09-570-767-44936	Sequence 44936, A
1299	73	3.0	374	4	US-09-252-991A-18114	Sequence 16, Appl	1373	72.5	3.0	226	2	US-08-190-199A-65	Sequence 65, Appl
1300	73	3.0	366	3	US-08-961-083-16	Sequence 16, Appl	1374	72.5	3.0	260	4	US-09-322-409-65	Sequence 65, Appl
1301	73	3.0	366	3	US-08-961-083-16	Sequence 16, Appl	1375	72.5	3.0	260	4	US-09-451-527-65	Sequence 65, Appl
1302	73	3.0	401	4	US-09-134-000C-4410	Sequence 4410, Ap	1376	72.5	3.0	295	3	US-09-002-298-5	Sequence 5, Appl1
1303	73	3.0	414	4	US-09-543-681A-4320	Sequence 4320, Ap	1377	72.5	3.0	312	4	US-09-481-277-5	Sequence 5, Appl1
1304	73	3.0	416	3	US-08-946-329A-17	Sequence 17, Appl	1378	72.5	3.0	312	4	US-09-110-279-3060	Sequence 3060, Ap
1305	73	3.0	416	3	US-08-567-357A-17	Sequence 17, Appl	1379	72.5	3.0	318	4	US-09-252-991A-23917	Sequence 23917, A
1306	73	3.0	416	3	US-08-729-743A-17	Sequence 17, Appl	1380	72.5	3.0	320	3	US-09-134-001C-4A04	Sequence 4A04, Ap
1307	73	3.0	416	3	US-08-349-498-17	Sequence 17, Appl	1381	72.5	3.0	338	3	US-08-722-184-8	Sequence 8, Appl1
1308	73	3.0	416	3	US-08-325-256-25	Sequence 25, Appl	1382	72.5	3.0	338	3	US-09-043-937A-12	Sequence 12, Appl
1309	73	3.0	416	4	US-09-704-917-18	Sequence 18, Appl	1383	72.5	3.0	347	4	US-09-902-540-10503	Sequence 10503, A
1310	73	3.0	416	4	US-09-151-999-18	Sequence 18, Appl	1384	72.5	3.0	375	4	US-09-818-780-23	Sequence 23, Appl
1311	73	3.0	416	4	US-09-418-221-17	Sequence 17, Appl	1385	72.5	3.0	383	2	US-08-558-269-6	Sequence 6, Appl1
1312	73	3.0	416	5	PCT-US95-15463-17	Sequence 17, Appl	1386	72.5	3.0	383	3	US-09-410-882-6	Sequence 6, Appl1
1313	73	3.0	416	5	PCT-US95-15463-17	Sequence 17, Appl	1387	72.5	3.0	410	3	US-09-352-990-16	Sequence 16, Appl
1314	73	3.0	416	4	US-09-583-110-2941	Sequence 2941, Ap	1388	72.5	3.0	410	4	US-09-755-630D-292	Sequence 292, App
1315	73	3.0	416	4	US-09-107-433-4452	Sequence 4452, Ap	1389	72.5	3.0	410	4	US-09-755-630D-292	Sequence 12, Appl
1316	73	3.0	416	4	US-09-489-039A-8380	Sequence 8380, Ap	1390	72.5	3.0	419	4	US-09-902-540-11960	Sequence 11960, A
1317	73	3.0	416	4	US-09-489-039A-8380	Sequence 5355, Ap	1391	72.5	3.0	423	2	US-08-290-731C-10	Sequence 10, Appl
1318	73	3.0	416	4	US-09-489-039A-12283	Sequence 12283, A	1392	72.5	3.0	423	3	US-09-134-001C-4717	Sequence 4717, Ap
1319	73	3.0	416	4	US-09-134-000C-5664	Sequence 5664, Ap	1393	72.5	3.0	433	1	US-08-700-359-20	Sequence 20, Appl
1320	73	3.0	416	4	US-09-134-000C-5664	Sequence 5862, Ap	1394	72.5	3.0	433	4	US-09-252-991A-23792	Sequence 23792, A
1321	73	3.0	416	4	US-09-583-110-3922	Sequence 23, Appl	1395	72.5	3.0	462	4	US-09-328-352-7472	Sequence 7472, Ap
1322	73	3.0	416	4	US-09-351-150A-23	Sequence 8380, Ap	1396	72.5	3.0	462	4	US-09-328-352-7472	Sequence 6749, Ap
1323	73	3.0	416	4	US-09-489-039A-8380	Sequence 24309, A	1397	72.5	3.0	462	4	US-09-328-352-7472	Sequence 5141, Ap
1324	73	3.0	416	4	US-09-252-991A-24309	Sequence 1096, Ap	1398	72.5	3.0	510	4	US-09-134-000C-5141	Sequence 24984, A
1325	73	3.0	522	4	US-09-538-092-1096	Sequence 25, Appl	1399	72.5	3.0	515	4	US-09-252-991A-24984	Sequence 2, Appl1
1326	73	3.0	524	4	US-09-549-519-25	Sequence 18, Appl	1400	72.5	3.0	520	4	US-09-564-808-2	Sequence 4, Appl1
1327	73	3.0	530	4	US-09-390-234-18	Sequence 18, Appl	1401	72.5	3.0	521	4	US-09-107-433-2996	Sequence 2996, Ap
1328	73	3.0	530	4	US-09-603-311-18	Sequence 1024, Ap	1402	72.5	3.0	531	4	US-09-583-110-3332	Sequence 3332, Ap
1329	73	3.0	535	4	US-09-710-279-1024	Sequence 5058, Ap	1403	72.5	3.0	534	4	US-09-107-532A-6549	Sequence 6549, Ap
1330	73	3.0	551	3	US-09-583-110-5058	Sequence 4191, Ap	1404	72.5	3.0	540	4	US-09-552-991A-18305	Sequence 18305, A
1331	73	3.0	551	3	US-09-134-001C-4191	Sequence 15245, A	1405	72.5	3.0	543	2	US-08-922-1708-10	Sequence 10, Appl
1332	73	3.0	556	2	US-09-902-540-15245	Sequence 2, Appl1	1406	72.5	3.0	543	3	US-09-071-7339-2	Sequence 2, Appl1
1333	73	3.0	556	2	US-08-392-806A-2	Sequence 2, Appl1	1407	72.5	3.0	543	3	US-09-260-0388-2	Sequence 2, Appl1
1334	73	3.0	556	3	US-09-257-490-2	Sequence 8, Appl1	1408	72.5	3.0	543	4	US-09-635-923-2	Sequence 2, Appl1
1335	73	3.0	625	4	US-09-602-864-17	Sequence 17, Appl	1409	72.5	3.0	543	4	US-09-487-716A-2	Sequence 2, Appl1
1336	73	3.0	630	4	US-09-485-529-8	Sequence 19386, A	1410	72.5	3.0	543	4	US-09-322-977-2	Sequence 2, Appl1
1337	73	3.0	630	4	US-09-252-991A-19386	Sequence 71920, Ap	1411	72.5	3.0	543	4	US-09-186-200-1	Sequence 10, Appl
1338	73	3.0	652	4	US-09-949-016-7320	Sequence 31942, Ap	1412	72.5	3.0	543	4	US-09-435-739-10	Sequence 3, Appl1
1339	73	3.0	652	4	US-09-252-991A-31942	Sequence 25444, A	1413	72.5	3.0	543	4	US-09-930-218-3	Sequence 2, Appl1
1340	73	3.0	662	4	US-09-252-991A-31942	Sequence 25444, A	1414	72.5	3.0	543	4	US-09-704-772A-2	Sequence 2, Appl1
1341	73	3.0	666	4	US-09-252-991A-25444								

1415 72.5 3.0 543 4 US-09-988-113-10 Sequence 10, Appl
1416 72.5 3.0 543 4 US-09-944-602-2 Sequence 2, Appl
1417 72.5 3.0 543 4 US-09-938-956-7 Sequence 7, Appl
1418 72.5 3.0 544 4 US-09-614-912-176 Sequence 176, App
1419 72.5 3.0 552 1 US-09-252-991A-17065 Sequence 17065, A
1420 72.5 3.0 552 3 US-08-116-098-2 Sequence 2, Appl
1421 72.5 3.0 552 3 US-08-687-590-32 Sequence 32, Appl
1422 72.5 3.0 554 4 US-09-438-185A-124 Sequence 124, App
1423 72.5 3.0 562 4 US-09-902-540-10175 Sequence 10175, A
1424 72.5 3.0 592 4 US-09-435-739-14 Sequence 14, Appl
1425 72.5 3.0 592 4 US-09-988-113-14 Sequence 11, Appl
1426 72.5 3.0 599 2 US-08-846-526-11 Sequence 2, Appl
1427 72.5 3.0 599 3 US-09-172-339-2 Sequence 22, Appl
1428 72.5 3.0 599 4 US-09-398-395A-22 Sequence 22, Appl
1429 72.5 3.0 599 4 US-09-887-586A-22 Sequence 22, Appl
1430 72.5 3.0 599 4 US-09-895-752-22 Sequence 22, Appl
1431 72.5 3.0 599 4 US-09-903-012B-22 Sequence 22, Appl
1432 72.5 3.0 599 4 US-09-900-797-22 Sequence 22, Appl
1433 72.5 3.0 616 4 US-09-252-991A-28137 Sequence 28137, A
1434 72.5 3.0 634 1 US-07-779-049-3 Sequence 3, Appl
1435 72.5 3.0 634 1 US-08-080-240-3 Sequence 3, Appl
1436 72.5 3.0 639 4 US-09-107-532A-4304 Sequence 4304, Ap
1437 72.5 3.0 643 4 US-09-602-864-13 Sequence 13, Appl
1438 72.5 3.0 646 1 US-08-441-139-14 Sequence 14, Appl
1439 72.5 3.0 646 4 US-09-919-039-11 Sequence 11, Appl
1440 72.5 3.0 652 4 US-09-134-000C-4855 Sequence 4855, Ap
1441 72.5 3.0 652 4 US-09-252-991A-18102 Sequence 18102, A
1442 72.5 3.0 688 4 US-09-902-540-14399 Sequence 14399, A
1443 72.5 3.0 752 4 US-09-585-858-26 Sequence 26, Appl
1444 72.5 3.0 752 4 US-10-270-878-26 Sequence 26, Appl
1445 72.5 3.0 757 4 US-09-538-092-520 Sequence 520, App
1446 72.5 3.0 816 4 US-09-134-000C-6157 Sequence 6157, Ap
1447 72.5 3.0 881 4 US-09-489-039A-13851 Sequence 13851, A
1448 72.5 3.0 890 4 US-09-513-783A-174 Sequence 174, App
1449 72.5 3.0 894 4 US-09-949-016-10605 Sequence 10605, A
1450 72.5 3.0 1014 1 US-09-134-000C-6265 Sequence 6265, Ap
1451 72.5 3.0 1153 4 US-08-097-997A-14 Sequence 14, Appl
1452 72.5 3.0 1157 4 US-09-949-016-9568 Sequence 9568, Ap
1453 72.5 3.0 1274 4 US-09-602-777A-360 Sequence 360, App
1454 72.5 3.0 1306 3 US-08-999-774A-13 Sequence 13, Appl
1455 72.5 3.0 1319 2 US-08-290-731C-2 Sequence 2, Appl
1456 72.5 3.0 1336 2 US-08-290-731C-6 Sequence 6, Appl
1457 72.5 3.0 1557 4 US-09-410-551B-27 Sequence 27, Appl
1458 72.5 3.0 1557 4 US-09-940-316B-27 Sequence 27, Appl
1459 72.5 3.0 2713 5 PCT-US96-01735-1 Sequence 1, Appl
1460 72.5 3.0 10182 3 US-09-134-001C-3159 Sequence 3159, Ap
1461 72.5 3.0 216 4 US-08-914-375C-2 Sequence 2, Appl
1462 72.5 3.0 245 4 US-09-543-681A-6428 Sequence 6428, Ap
1463 72.5 3.0 262 4 US-09-252-991A-29803 Sequence 29803, A
1464 72.5 3.0 276 3 US-08-659-254-2 Sequence 2, Appl
1465 72.5 3.0 297 4 US-09-543-681A-7800 Sequence 7800, Ap
1466 72.5 3.0 318 4 US-09-602-777A-6 Sequence 6, Appl
1467 72.5 3.0 319 4 US-09-602-777A-4 Sequence 4, Appl
1468 72.5 3.0 323 4 US-09-543-681A-5244 Sequence 5244, Ap
1469 72.5 3.0 337 4 US-09-902-540-12246 Sequence 12246, A
1470 72.5 3.0 344 4 US-09-134-000C-5022 Sequence 5022, Ap
1471 72.5 3.0 372 4 US-09-248-796A-17994 Sequence 17994, A
1472 72.5 3.0 378 4 US-09-107-532A-6328 Sequence 6328, Ap
1473 72.5 3.0 379 4 US-09-134-000C-6027 Sequence 6027, Ap
1474 72.5 3.0 405 3 US-09-434-774-2 Sequence 2, Appl
1475 72.5 3.0 408 4 US-09-723-546-13 Sequence 13, Appl
1476 72.5 3.0 411 4 US-08-311-731A-369 Sequence 369, App
1477 72.5 3.0 413 4 US-09-489-039A-12535 Sequence 12535, A
1478 72.5 3.0 433 4 US-09-962-357-3 Sequence 3, Appl
1479 72.5 3.0 443 4 US-09-538-092A-494 Sequence 494, App
1480 72.5 3.0 465 4 US-09-252-991A-21223 Sequence 21223, A
1481 72.5 3.0 496 4 US-09-252-991A-21949 Sequence 21949, A
1482 72.5 3.0 504 4 US-09-540-336A-3662 Sequence 3662, Ap
1483 72.5 3.0 508 4 US-09-489-039A-8801 Sequence 8801, Ap
1484 72.5 3.0 516 3 US-08-888-949-17 Sequence 17, Appl
1485 72.5 3.0 516 3 US-08-888-950-17 Sequence 17, Appl
1486 72.5 3.0 516 3 US-09-262-758-17 Sequence 17, Appl
1487 72.5 3.0 516 4 US-09-885-876-17 Sequence 17, Appl

1488 72 3.0 516 4 US-09-885-901-17 Sequence 17, Appl
1489 72 3.0 520 4 US-09-731-393-17 Sequence 17, Appl
1490 72 3.0 526 4 US-09-257-825B-20 Sequence 20, Appl
1491 72 3.0 525 4 US-09-248-796A-15927 Sequence 15927, A
1492 72 3.0 529 1 US-08-484-815-12 Sequence 12, Appl
1493 72 3.0 529 1 US-08-888-949-12 Sequence 12, Appl
1494 72 3.0 529 3 US-08-888-950-12 Sequence 12, Appl
1495 72 3.0 529 3 US-09-262-758-12 Sequence 12, Appl
1496 72 3.0 529 4 US-09-885-876-12 Sequence 12, Appl
1497 72 3.0 529 4 US-09-351-150A-3 Sequence 3, Appl
1498 72 3.0 529 4 US-09-885-901-12 Sequence 12, Appl
1499 72 3.0 529 4 US-09-731-393-12 Sequence 12, Appl
1500 72 3.0 529 4 US-09-882-694B-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-188-930-339
Sequence 339, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Iorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Mutison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.101c1
CURRENT APPLICATION NUMBER: US/09/188.930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
ORGANISM: Mouse
US-09-188-930-339
Query Match 97.5%; Score 2362; DB 3; Length 469;
Best Local Similarity 97.2%; Pred. No. 1.6e-228;
Matches 456; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 MLCGLVVPVIGAGQTEFOYFESKGLPAELKSIIFKLSVFIPSOEFSTYRWKQIVAGD 60
Db 1 MLCGLVVPVIGAGQTEFOYFESKGLPAELKSIIFKLSVFIPSOEFSTYRWKQIVAGD 60
QY 61 KDLDGQIDFEFPHYIYLDHDKKRLRVFKILDKKNDGRIDAOETMOSLRDVGKISEQAE 120
Db 61 KDLDGQIDFEFPHYIYLDHDKKRLRVFKILDKKNDGRIDAOETMOSLRDVGKISEQAE 120
QY 121 KIILKSDKXGNTWTIDNNEWRDYLHPVENIPETIILYWKASTIFDVGENTLVPEPTVEE 180
Db 121 KIILKSDKXGNTWTIDNNEWRDYLHPVENIPETIILYWKASTIFDVGENTLVPEPTVEE 180
QY 181 ROTGMMWRHLVAGGAGAVSRCTAPLDRILKVLMOVYASRNNMGIVGFTOMIREGAR 240
Db 181 ROTGMMWRHLVAGGAGAVSRCTAPLDRILKVLMOVYASRNNMGIVGFTOMIREGAR 240
QY 241 SLWRGNGINVLKTAPEBSAIFPMAYEQIKRLVGSQDOTLRHRELVAGSLAGTAIOSSITP 300
Db 241 SLWRGNGINVLKTAPEBSAIFPMAYEQIKRLVGSQDOTLRHRELVAGSLAGTAIOSSITP 300
QY 301 MEVLKTRMALRKTOGYSGLMDCCARRIAREGVAFYGYVPMNGIIPYAGIDLAVETL 360
Db 301 MEVLKTRMALRKTOGYSGLMDCCARRIAREGVAFYGYVPMNGIIPYAGIDLAVETL 360
QY 361 KXNMLQHYAVNSADPGVFVLLACGTMSSTGOLASYPALAVRTMKAQASIEGAPVYWS 420
Db 361 KXNMLQHYAVNSADPGVFVLLACGTMSSTGOLASYPALAVRTMKAQASIEGAPVYWS 420

QY 421 SLFKHILRTGAGFLYRGLAPNFMKVI PAVISIVYVENIKITLGVQSR 469
DB 421 SLFKQILRTGAGFLYRGLAPNFMKVI PAVISIVYVENIKITLGVQSR 469

RESULT 2

US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-339

Query Match 97.5%; Score 2362; DB 4; Length 469;
Best Local Similarity 97.2%; Pred. No. 1,6e-228;
Matches 456; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MLCCLYVPVIGBAQTEFOYFESKGLPAELKSI FKLVSFIPSOEFSTYRQMKIYQAGD 60
DB 1 MLCCLYVPVIGBAQTEFOYFESKGLPAELKSI FKLVSFIPSOEFSTYRQMKIYQAGD 60
QY 61 KDLDGQLDPEEFVHYI QDHEKKRLVFKI LDKNDRIDAQEI MQSLRDLGVKISQOAE 120
DB 61 KDLDGQLDPEEFVHYI QDHEKKRLVFKI LDKNDRIDAQEI MQSLRDLGVKISQOAE 120
QY 121 KILKSMXKNGTMTIDNNEEMRDYHLHPVENIP EILLYWKHSTI FDVGENLTVDEFTVEE 180
DB 121 KILKSMXKNGTMTIDNNEEMRDYHLHPVENIP EILLYWKHSTI FDVGENLTVDEFTVEE 180
QY 181 ROTGMMWRHLVAGGAGAVSRTCTAPLDRLKVL MQVHASRNNMGIVGFTQMI REGGAR 240
DB 181 ROTGMMWRHLVAGGAGAVSRTCTAPLDRLKVL MQVHASRNNMGIVGFTQMI REGGAR 240
QY 241 SLWRGNGINVLKTIAPESAIKFMAYEQIKRLVGS DQETLRIHERLVAGSLAGAI AQSSTYP 300
DB 241 SLWRGNGINVLKTIAPESAIKFMAYEQIKRLVGS DQETLRIHERLVAGSLAGAI AQSSTYP 300
QY 301 MEVLKTRMALRKQVSGMIDCARILABEGVAAFYGY PNMGLIIPYAGIDLAVYETL 360
DB 301 MEVLKTRMALRKQVSGMIDCARILABEGVAAFYGY PNMGLIIPYAGIDLAVYETL 360
QY 361 KNAWLOHYAVNSADPGVFVLLACGTMSSTGOLAS YPLALVTRRMOQASIEGAPETVMS 420
DB 361 KNAWLOHYAVNSADPGVFVLLACGTMSSTGOLAS YPLALVTRRMOQASIEGAPETVMS 420
QY 421 SLFKHILRTGAGFLYRGLAPNFMKVI PAVISIVYVENIKITLGVQSR 469
DB 421 SLFKQILRTGAGFLYRGLAPNFMKVI PAVISIVYVENIKITLGVQSR 469

RESULT 3

US-09-188-930-142
; Sequence 142, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew
; APPLICANT: Murison, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 142
; LENGTH: 312
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-142

Query Match 65.5%; Score 1588; DB 3; Length 312;
Best Local Similarity 97.8%; Pred. No. 5.7e-151;
Matches 305; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLCCLYVPVIGBAQTEFOYFESKGLPAELKSI FKLVSFIPSOEFSTYRQMKIYQAGD 60
DB 1 MLCCLYVPVIGBAQTEFOYFESKGLPAELKSI FKLVSFIPSOEFSTYRQMKIYQAGD 60
QY 61 KDLDGQLDPEEFVHYI QDHEKKRLVFKI LDKNDRIDAQEI MQSLRDLGVKISQOAE 120
DB 61 KDLDGQLDPEEFVHYI QDHEKKRLVFKI LDKNDRIDAQEI MQSLRDLGVKISQOAE 120
QY 121 KILKSMXKNGTMTIDNNEEMRDYHLHPVENIP EILLYWKHSTI FDVGENLTVDEFTVEE 180
DB 121 KILKSMXKNGTMTIDNNEEMRDYHLHPVENIP EILLYWKHSTI FDVGENLTVDEFTVEE 180
QY 181 ROTGMMWRHLVAGGAGAVSRTCTAPLDRLKVL MQVHASRNNMGIVGFTQMI REGGAR 240
DB 181 ROTGMMWRHLVAGGAGAVSRTCTAPLDRLKVL MQVHASRNNMGIVGFTQMI REGGAR 240
QY 241 SLWRGNGINVLKTIAPESAIKFMAYEQIKRLVGS DQETLRIHERLVAGSLAGAI AQSSTYP 300
DB 241 SLWRGNGINVLKTIAPESAIKFMAYEQIKRLVGS DQETLRIHERLVAGSLAGAI AQSSTYP 300
QY 301 MEVLKTRMALRK 312
DB 301 MEVLKTRMALRK 312

RESULT 4

US-09-312-283C-142
; Sequence 142, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Murison, Rene
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-142

Query Match 65.5%; Score 1588; DB 4; Length 312;
Best Local Similarity 97.8%; Pred. No. 5.7e-151;
Matches 305; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Query 1 MLCLCLVPLVIGAEOTFEYFESKGLPAELKISFVLPSOEFSTYRQKQKIYAGD 60
Db 1 MLCLCLVPLVAGAOQTEFQFESKGLPELKLISFVLPSOEFSTYRQKQKIYAGD 60
Query 61 KDLQDGLDFEFVHYLDHEKRLVFKILDKKNDGIDAEIQSLRDJGVKISEQOAE 120
Db 61 KDLQDGLDFEFVHYLDHEKRLVFKILDKKNDGIDAEIQSLRDJGVKISEQOAE 120
Query 121 KILKSMKNGTMTIDNEMRDYHLHPVENPELILYWKSTIDVGENLTVPDEFVVEE 180
Db 121 KILKSMKNGTMTIDNEMRDYHLHPVENPELILYWKSTIDVGENLTVPDEFVVEE 180
Query 181 ROTGMMRHVAGGAGAVSRTCTAPLDRKLVLMQVARSNNMGIVGFTQMIREGGAR 240
Db 181 ROTGMMRHVAGGAGAVSRTCTAPLDRKLVLMQVARSNNMGIVGFTQMIREGGAR 240
Query 241 SLWRNGINVLKIAPESAIKFMAVEQIKRLVGSDOETLRHERLVAGSLAGAIQSSIYP 300
Db 241 SLWRNGINVLKIAPESAIKFMAVEQIKRLVGSDOETLRHERLVAGSLAGAIQSSIYP 300
Query 301 MEVLKTMALRK 312
Db 301 MEVLKTMALRK 312

RESULT 5
US-09-270-767-44809
; Sequence 44809, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OR INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 44809
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44809

Query Match 28.2%; Score 682.5; DB 4; Length 376;
Best Local Similarity 54.1%; Pred. No. 8.9e-60;
Matches 125; Conservative 42; Mismatches 61; Indels 3; Gaps 1;

Query 44 EFTYRQMKQKIYQAGDKDLQDGLDFEFVHYLDHEKRLVFKILDKKNDGIDAEI 103
Db 148 EFTGLSVYAKFPLQOSDKDQSGNVPFALHYVREHEKNLVLPQSHDKRDKVDLEL 207
Query 104 MQLSRDGVKISEQOAEKILKSMKNGTMTIDNEMRDYHLHPVENPELILYWKSTI 163
Db 208 ISAFKDLGLIDMEARNLLTRMDKQSLNLSFEMWDFMLABSTDIHDLKFMRSSTY 267
Query 164 FIDVGENLTVPDEFVVEEYRQGMTRHVLVAGGAGAVSRTCTAPLDRKLVLMQVARSNN 223
Db 268 LDIQEDMNVPDDFQKEMQGLMWRHLVAGGIAAVSRTCTAPLDRKLVLMQVARSNN 324
Query 224 MGIVGFTQMIREGGARSLWRNGINVLKIAPESAIKFMAVEQIKRLVGS 274
Db 325 MGISECMHMLNBGSGSRSMRNGINVLKIAPEFAFPAVEQMKRLRGD 375

RESULT 6
US-09-796-766-20
; Sequence 20, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OR INVENTION: BRITTLE-1 HOMOLOGS

FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-796-766-20

Query Match 17.6%; Score 427.5; DB 4; Length 289;
Best Local Similarity 34.2%; Pred. No. 2.5e-34;
Matches 96; Conservative 64; Mismatches 104; Indels 17; Gaps 7;

Query 188 RHLVAGGAGAVSRTCTAPLDRKLVLMQVARSNNMGIVGFTQMIREGGARSLWRNG 247
Db 10 KRLISGIGAGAVSRTVVAPELIRTHLMVGSNGNSSTEV--FDSIMKNGMTGLFRGNL 66
Query 248 INVLIAPESAIKFMAYEQIKRLV--GSDOETLRHERLVAGSLAGAIQSSIYPMEVL 304
Db 67 VNVIRVAPSKAIBIEFADTKKELTPKSGEOKIPPLPSVAGFAVGSSTLCTYPELI 126
Query 305 KTRMALRKTQYSGMLDCARRILAREGVAIFYGVNMLGIIPYAGIDLAVVETLKNAM 364
Db 127 KTRLITQR-GVYDNFLHAFKIVREBPALYGLTSLGVPYAAITNPAITTLKKVY 185
Query 365 LQHYAVNSAD--PGVFLAACGTMSSTCGQASYPALAVTRMQAQSISGAPEV--TMS 420
Db 186 KQMFETNEIGNVPTLLIGSAAIAISF---ATPPLVAKHMQVGA--VGRKRYTQML 239
Query 421 SLFKHILRTGAGLIRGLAPNPMKVIYPAVSISYVYENIK 461
Db 240 HALTLIEDRGVGLYRGLGSPCKLVPAAGISFMCYEACK 280

RESULT 7
US-09-796-766-18
; Sequence 18, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafaleki, Antoni
; TITLE OR INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BB1157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-796-766-18

Query Match 17.3%; Score 418.5; DB 4; Length 433;
Best Local Similarity 28.7%; Pred. No. 4e-33;
Matches 116; Conservative 64; Mismatches 149; Indels 75; Gaps 10;

Query 119 AEKILKSMKNGTMTIDNEMRDYHLHPVENPELILYV----- 158

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Db      6 AATTMTYKNNRASILVMDKKM-----ILRPV---PEVAFPMSSQPESSLDPPRALFASV 58
Qy      159 -----KSTFDVGENLTVPDEFTYEEROTM----- 165
Db      59 GLSLSHCAPVAREBHDKARPADDVAHQIAGAGVQKAKKAKKQOLSLRKRVKI 118
Qy      186 ---WMRLVAVGGAGAVSRTCTAPLDRILKYLMOVHASRSNNMGI VGGFTOMIREGARSL 242
Db      119 GNPRLRLVSGALAGAVSRTFVAPLETIRTHLMVSGGADSM--AGVFRIMITEGMPGL 176
Qy      243 WRNGINVLKIAPESAIKFMAIEQIKLV--GSDDETLRIHERLVAGSLAGIAQSSIT 299
Db      177 FRNAVAVLVAPASKALEHFTYDPAKKYLLPEEAGEBPAAKVIPTPLVAGALAGASTLCTY 236
Qy      300 PHEVLKTRMALRKTOGYSGLDCARRILAREGVAAFKGVYPMNLGIIIPAGIDLAVYET 359
Db      237 PHELVKTRLTIER-DYVDNLILHAFVKIVRDEGPEGLYRGLAPSLIGVVPYAAANFVAYET 235
Qy      360 LKNAMLQHYAVNSADPGVFVLLACGTMSTCGOLASYPALVTRMQOASIEGAPETM 419
Db      296 LRGVYR--ASGKEVGNVPTLLIGSAAALASTATPELEVARKOMQVGA--VGRQVYK 351
Qy      420 SSLPKH--ILRTGAFGLYRGLAPNFMKVI PAVSISVYVENLK 461
Db      352 NVLHMYCILEKEGTAGLYRGLPSCIKMPAGISFMCTEACK 395
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RESULT 8

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US-09-796-766-14
; Sequence 14, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BBI157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Glycine max
US-09-796-766-14
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Query Match 17.2%; Score 417; DB 4; Length 272;

Best Local Similarity 34.0%; Pred. No. 2.6e-33;

Matches 91; Conservative 60; Mismatches 107; Indels 10; Gaps 5;

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Qy      197 GAVSRTCTAPLDRILKYLMOVHASRSNNMGI VGGFTOMIREGARSLIRGNGINVLKIAPE 256
Db      3 GAVSRTAVAPLETIRTHLMVSGCHSTIYV--FQSIPTEDQMGGLRGNFVNITIRVAPS 59
Qy      257 SAIKFAVAEQIKRLV---SDOETLRIHERLVAGSLAGIAQSSIYPMELKTRMALRKT 313
Db      60 KALELFAVDYVKKQSLKPEQPIPIPPESINGAVAGVSTICTYVLELTKRLTLVQR- 118
Qy      314 GOYSGLDCARRILAREGVAAFKGVYPMNLGIIIPAGIDLAVYETIKNAMLQHYAVNSA 373
Db      119 GYVKNLIDAFVRIVQEEGPALRYRGLAPSLIGVLPYATVYFVDTLRKAYKK--AFKE 176
Qy      374 DPGVFVLLACGTMSTCGOLASYPALVTRMQOASIEGAPETMSLFXHILRTGAF 433
Db      177 EIGNVMTLLIGSAAAGISSATPELEVARKOMQGA-LNGROYGNMLHALVSLIEKGVG 235
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Qy      434 GLYRGLAPNFMKVI PAVSISVYVENLK 461
Db      236 GLYRGLGPSCLKVPAAGISFMCTEACK 263
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RESULT 9

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US-09-796-766-21
; Sequence 21, Application US/09796766
; Patent No. 6660850
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lightner, Jonathan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: BRITTLE-1 HOMOLOGS
; FILE REFERENCE: BBI157 US CIP
; CURRENT APPLICATION NUMBER: US/09/796,766
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/668884
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/06583
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079420
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Zea mays
US-09-796-766-21
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Query Match 17.1%; Score 415.5; DB 4; Length 436;

Best Local Similarity 35.0%; Pred. No. 8e-33;

Matches 104; Conservative 58; Mismatches 118; Indels 17; Gaps 8;

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Qy      173 PDEFTYBEROTGMWMLHVLVAGGAGVSRCTAPLDRILKYLMOVHASRSNNMGI VGGFTQ 232
Db      123 PEEGQODROPAP--ARLVSGALAGAVSRTFVAPLETIRTHLMVGSIGVDSM--AGVFW 178
Qy      233 MIREGARSLMRNGINVLKIAPESAIKFMAIEQIKRLV---GSDDETLRIHERLVAGSL 289
Db      179 IMONBEWTLFRNAVAVLVAPASKALEHFTYDPAKKYLLPEEAGEBPAAKVIPTPLVAGAL 238
Qy      290 AGAIAQSSIYPMELKTRMALRKTCQYSGMLDCARRILAREGVAAFKGVYPMNLGIIIPY 349
Db      239 AGFASLTCTYPMELITRVTIER-DYVDNAHAFVKILNDEGSELYRGLTPELVGVY 297
Qy      350 AGIDLAVYETIKNAMLQHYAVN-SADPGVFVLLACGTMSTCGOLASYPALVTRMQAO 408
Db      298 AACNFYAYETLTKLYRRATGRRPADVGPVATLLIGSAAALASATPPELEVARKOMQV 357
Qy      409 ASIEGAPETMSLFGH---ILRTGAFGLYRGLAPNFMKVI PAVSISVYVENLK 461
Db      358 A--VGRROYONVL--HAIYCIKKEGAGSLYRGLPSCIKMPAGIAFMCTEACK 410
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RESULT 10

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US-09-270-767-43371
; Sequence 43371, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 43371
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
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US-09-270-767-43371

Query Match 14.6%; Score 354; DB 4; Length 142;
Best Local Similarity 54.7%; Pred. No. 1.9e-27;
Matches 76; Conservative 17; Mismatches 28; Indels 18; Gaps 2;

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DB 3 ILIPAGIDLAVETLKRRIYANHD-NNEQPSFLVLLACGTSSTLQGLCSYPLVLRTRL 61

QY 406 QAAQ-----SIEGAEVTVMSLFFKHLRTGAFGLYRGLAPNFMKVIP 448

DB 62 QAAQAEITANQKRTQIPLKSSDAHSGEETMTGLFRKIVRQEGTLGLYRGITTPFLKVL 121

QY 449 AVSISIVYVENLKTTLGVQ 467

DB 122 AVSISIVYVEYTSRALGIK 140

RESULT 11

US-09-270-767-58719

Sequence 58719, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270.767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 58719

LENGTH: 142

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-58719

Query Match 14.6%; Score 354; DB 4; Length 142;

Best Local Similarity 54.7%; Pred. No. 1.9e-27;

Matches 76; Conservative 17; Mismatches 28; Indels 18; Gaps 2;

QY 346 IIPYAGIDLAVERTLKNAWLOHYAVNSADPGVFLVLLACGTSSTCGOLASYPALVTRTM 405

DB 3 ILIPAGIDLAVETLKRRIYANHD-NNEQPSFLVLLACGTSSTLQGLCSYPLVLRTRL 61

QY 406 QAAQ-----SIEGAEVTVMSLFFKHLRTGAFGLYRGLAPNFMKVIP 448

DB 62 QAAQAEITANQKRTQIPLKSSDAHSGEETMTGLFRKIVRQEGTLGLYRGITTPFLKVL 121

QY 449 AVSISIVYVENLKTTLGVQ 467

DB 122 AVSISIVYVEYTSRALGIK 140

RESULT 12

US-09-796-766-10

Sequence 10, Application US/09796766

Patent No. 6660850

GENERAL INFORMATION:

APPLICANT: Allen, Steve

TITLE OF INVENTION: BRITTLE-1 HOMOLOGS

FILE REFERENCE: BB1157 US CIP

CURRENT APPLICATION NUMBER: US/09/796.766

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Microsoft Office 97

US-09-270-767-32789

Query Match 13.1%; Score 318.5; DB 4; Length 227;
Best Local Similarity 38.5%; Pred. No. 1.5e-23;
Matches 85; Conservative 38; Mismatches 85; Indels 13; Gaps 8;

QY 252 KIAPESAIKFMAYEQRKLVGSDOE-TLRHERLVAGSLAGATAOSSIPMEVLEKTRMAL 310

DB 1 RIVPYALIOFTAHQWRRIIHDKDGINTKGRFLAGSLAGITSQSILTYPLDLARAMAV 60

QY 311 -RKTQYSGMLDCARRILAREGVAAYKGYVPMIGIIPYAGIDLAVERTLKNAWLOHY 368

DB 61 TDRYTG-YRTLQVFTKIWEBEGPRTLFRGYMATVLGVIYAGTSFPTYETLKEEYVE-- 117

QY 369 AVNSADPGVFLVLLACGTSSTCGOLASYPALVTRTMQAO-----ASIEGAEVTVMSLFFK 424

DB 118 VGNKNTLVLSLAFGAAAGQATASYPDLIVRRRQTRVATAGDGRYPTL-LETLVK 176

QY 425 HIARTEGA-FGLYRGLAPNFMKVIPAVSISIVYVENLKTTL 464

DB 177 -IYREBGVKNQFYKGLSMNWKIPAVGISFSFYDLIKAWL 216

US-09-270-767-32789

Query Match 13.1%; Score 318.5; DB 4; Length 227;

Best Local Similarity 38.5%; Pred. No. 1.5e-23;

Matches 85; Conservative 38; Mismatches 85; Indels 13; Gaps 8;

QY 252 KIAPESAIKFMAYEQRKLVGSDOE-TLRHERLVAGSLAGATAOSSIPMEVLEKTRMAL 310

DB 1 RIVPYALIOFTAHQWRRIIHDKDGINTKGRFLAGSLAGITSQSILTYPLDLARAMAV 60

QY 311 -RKTQYSGMLDCARRILAREGVAAYKGYVPMIGIIPYAGIDLAVERTLKNAWLOHY 368

DB 61 TDRYTG-YRTLQVFTKIWEBEGPRTLFRGYMATVLGVIYAGTSFPTYETLKEEYVE-- 117

QY 369 AVNSADPGVFLVLLACGTSSTCGOLASYPALVTRTMQAO-----ASIEGAEVTVMSLFFK 424

DB 118 VGNKNTLVLSLAFGAAAGQATASYPDLIVRRRQTRVATAGDGRYPTL-LETLVK 176

QY 425 HIARTEGA-FGLYRGLAPNFMKVIPAVSISIVYVENLKTTL 464

DB 177 -IYREBGVKNQFYKGLSMNWKIPAVGISFSFYDLIKAWL 216

US-09-270-767-32789

Query Match 13.1%; Score 318.5; DB 4; Length 227;

Best Local Similarity 38.5%; Pred. No. 1.5e-23;

Matches 85; Conservative 38; Mismatches 85; Indels 13; Gaps 8;

QY 252 KIAPESAIKFMAYEQRKLVGSDOE-TLRHERLVAGSLAGATAOSSIPMEVLEKTRMAL 310

DB 1 RIVPYALIOFTAHQWRRIIHDKDGINTKGRFLAGSLAGITSQSILTYPLDLARAMAV 60

QY 311 -RKTQYSGMLDCARRILAREGVAAYKGYVPMIGIIPYAGIDLAVERTLKNAWLOHY 368

DB 61 TDRYTG-YRTLQVFTKIWEBEGPRTLFRGYMATVLGVIYAGTSFPTYETLKEEYVE-- 117

QY 369 AVNSADPGVFLVLLACGTSSTCGOLASYPALVTRTMQAO-----ASIEGAEVTVMSLFFK 424

DB 118 VGNKNTLVLSLAFGAAAGQATASYPDLIVRRRQTRVATAGDGRYPTL-LETLVK 176

QY 425 HIARTEGA-FGLYRGLAPNFMKVIPAVSISIVYVENLKTTL 464

DB 177 -IYREBGVKNQFYKGLSMNWKIPAVGISFSFYDLIKAWL 216

US-09-270-767-32789

Query Match 13.1%; Score 318.5; DB 4; Length 227;

Best Local Similarity 38.5%; Pred. No. 1.5e-23;

Matches 85; Conservative 38; Mismatches 85; Indels 13; Gaps 8;

QY 252 KIAPESAIKFMAYEQRKLVGSDOE-TLRHERLVAGSLAGATAOSSIPMEVLEKTRMAL 310

DB 1 RIVPYALIOFTAHQWRRIIHDKDGINTKGRFLAGSLAGITSQSILTYPLDLARAMAV 60

QY 311 -RKTQYSGMLDCARRILAREGVAAYKGYVPMIGIIPYAGIDLAVERTLKNAWLOHY 368

DB 61 TDRYTG-YRTLQVFTKIWEBEGPRTLFRGYMATVLGVIYAGTSFPTYETLKEEYVE-- 117

QY 369 AVNSADPGVFLVLLACGTSSTCGOLASYPALVTRTMQAO-----ASIEGAEVTVMSLFFK 424

DB 118 VGNKNTLVLSLAFGAAAGQATASYPDLIVRRRQTRVATAGDGRYPTL-LETLVK 176

QY 425 HIARTEGA-FGLYRGLAPNFMKVIPAVSISIVYVENLKTTL 464

DB 177 -IYREBGVKNQFYKGLSMNWKIPAVGISFSFYDLIKAWL 216

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OM protein - protein search, using sw model

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(without alignments)
1144.354 Million cell updates/sec

Perfect score: 2423
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Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27	2423	100.0	469	10	US-09-997-428-289 Sequence 289, App
128	2423	100.0	469	14	US-10-063-742-58 Sequence 58, Appl
221	2423	100.0	469	17	US-10-972-317-58 Sequence 58, Appl
222	2362	97.5	469	10	US-09-866-050A-339 Sequence 339, Appl
223	1588	65.5	469	10	US-09-866-050A-142 Sequence 142, App
224	1554	64.1	468	15	US-10-380-727-26 Sequence 26, Appl
225	1536	63.4	468	15	US-10-403-161-54 Sequence 54, Appl
226	1501	61.9	477	9	US-09-777-921A-2 Sequence 2, Appl
227	1501	61.9	477	15	US-10-698-489-2 Sequence 4, Appl
228	1494	61.7	475	9	US-09-777-921A-4 Sequence 4, Appl
229	1494	61.7	475	15	US-10-698-489-4 Sequence 4, Appl
230	1469	60.6	384	15	US-10-094-749-1789 Sequence 1789, Ap

231	1308	54.0	410	9	US-09-777-921A-5 Sequence 5, Appl
232	1308	54.0	410	15	US-10-698-489-5 Sequence 5, Appl
233	1308	54.0	411	16	US-10-408-765A-765 Sequence 765, App
234	1123	46.3	342	9	US-09-777-921A-6 Sequence 6, Appl
235	1123	46.3	342	15	US-10-698-489-6 Sequence 6, Appl
236	1120.5	46.2	222	14	US-10-116-255-30 Sequence 30, Appl
237	1030.5	42.5	531	15	US-10-369-493-6939 Sequence 6939, Ap
238	962.5	39.7	379	9	US-09-810-673A-4 Sequence 4, Appl
239	962.5	39.7	379	14	US-10-395-242-4 Sequence 4, Appl
240	920	38.0	332	9	US-09-810-673A-2 Sequence 2, Appl
241	920	38.0	332	14	US-10-395-242-2 Sequence 2, Appl
242	902	37.2	300	9	US-09-810-673A-6 Sequence 6, Appl
243	902	37.2	300	14	US-10-395-242-6 Sequence 6, Appl
244	858	35.4	169	14	US-10-116-255-31 Sequence 31, Appl
245	846	34.9	515	16	US-10-437-963-145987 Sequence 145987, A
246	831	34.3	413	15	US-10-425-114-55333 Sequence 55333, A
247	824.5	34.0	473	15	US-10-424-579-245081 Sequence 245081, A
248	811	33.5	170	11	US-09-764-875-690 Sequence 690, App
249	800	33.0	400	15	US-10-424-559-160423 Sequence 160423, A
250	770.5	31.8	502	16	US-10-425-115-296312 Sequence 296312, A
251	722.5	29.8	337	16	US-10-425-115-294578 Sequence 294578, A
252	679	28.0	222	15	US-10-108-260A-4574 Sequence 4574, Ap
253	652	26.9	330	15	US-10-425-114-51224 Sequence 51224, A
254	579	23.9	244	9	US-09-764-875-693 Sequence 693, App
255	575	23.7	244	11	US-09-764-881-138 Sequence 138, App
256	575	23.7	244	10	US-09-764-881-138 Sequence 108, App
257	575	23.7	244	11	US-09-764-875-1008 Sequence 108, App
258	575	23.7	244	15	US-10-242-747-138 Sequence 138, App
259	575	23.7	244	15	US-10-158-057-202 Sequence 202, App
260	566	23.4	125	9	US-09-764-881-135 Sequence 135, App
261	566	23.4	125	10	US-09-764-881-135 Sequence 105, App
262	566	23.4	125	11	US-09-764-875-1005 Sequence 1005, App
263	566	23.4	125	15	US-10-242-747-135 Sequence 135, App
264	566	23.4	125	15	US-10-158-057-199 Sequence 199, App
265	546.5	22.6	151	9	US-09-810-673A-5 Sequence 5, Appl
266	546.5	22.6	151	14	US-10-395-242-5 Sequence 5, Appl
267	533	22.0	345	15	US-10-424-559-221235 Sequence 221235, A
268	532	22.0	343	16	US-10-425-115-279923 Sequence 279923, A
269	531	21.9	335	16	US-10-425-115-279930 Sequence 279930, A
270	531	21.9	331	15	US-10-425-115-56333 Sequence 56333, A
271	521	21.5	355	16	US-10-437-963-184488 Sequence 184488, A
272	520.5	21.5	352	15	US-10-424-559-221242 Sequence 221242, A
273	518	21.4	355	16	US-10-767-701-45663 Sequence 45663, A
274	510	21.0	251	15	US-10-424-559-243469 Sequence 243469, A
275	500	20.6	188	9	US-09-810-673A-7 Sequence 7, Appl
276	500	20.6	188	14	US-10-395-242-7 Sequence 7, Appl
277	485.5	20.0	310	15	US-10-425-114-65685 Sequence 65685, A
278	482.5	19.9	337	16	US-10-425-115-282671 Sequence 282671, A
279	479	19.8	438	15	US-10-369-493-2504 Sequence 2504, App
280	471	19.4	366	16	US-10-437-963-124423 Sequence 124423, A
281	464	19.1	357	16	US-10-437-963-160189 Sequence 160189, A
282	456.5	18.8	305	15	US-10-424-559-281886 Sequence 281886, A
283	452.5	18.7	305	16	US-10-437-963-106088 Sequence 106088, A
284	452.5	18.7	206	15	US-10-425-114-42509 Sequence 42509, A
285	450.5	18.6	332	16	US-10-478-758-7 Sequence 7, Appl
286	442.5	18.3	337	16	US-10-739-930-6760 Sequence 6760, App
287	441.5	18.2	334	15	US-10-424-559-237118 Sequence 237118, A
288	436.5	18.0	333	15	US-10-424-559-222460 Sequence 222460, A
289	436	18.0	330	15	US-10-424-559-237117 Sequence 237117, A
290	429.5	17.7	345	16	US-10-437-963-149695 Sequence 149695, A
291	428.5	17.7	332	16	US-10-425-115-349270 Sequence 349270, A
292	427.5	17.6	289	9	US-09-796-765-20 Sequence 20, Appl
293	427.5	17.6	289	15	US-10-659-199-20 Sequence 20, Appl
294	426.5	17.6	415	16	US-10-437-963-122416 Sequence 122416, A
295	423.5	17.5	336	15	US-10-369-493-22510 Sequence 22510, A
296	418.5	17.3	433	9	US-09-796-766-18 Sequence 18, Appl
297	418.5	17.3	433	15	US-10-659-199-18 Sequence 18, Appl
298	417.5	17.2	329	9	US-10-425-115-344638 Sequence 344638, A
299	417	17.2	222	9	US-09-796-766-14 Sequence 14, Appl
300	417	17.2	272	15	US-10-659-199-14 Sequence 14, Appl
301	415.5	17.1	351	20	US-11-021-464-12 Sequence 12, Appl
302	415.5	17.1	436	9	US-09-796-766-21 Sequence 21, Appl
303	415.5	17.1	436	15	US-10-659-199-21 Sequence 21, Appl

304	415.5	17.1	436	20	US-11-021-464-8	Sequence 8, Appl1	377	325	13.4	405	15	US-10-425-114-73030	Sequence 73030, A
305	414.5	17.1	439	15	US-10-425-114-50902	Sequence 50902, A	378	325	13.4	412	15	US-10-425-114-45020	Sequence 45020, A
306	414.5	17.1	440	15	US-10-425-114-65995	Sequence 65995, A	379	325	13.4	413	15	US-10-425-114-66171	Sequence 66171, A
307	414.5	17.1	440	15	US-10-425-114-52535	Sequence 52535, A	380	325	13.4	413	15	US-10-425-114-73083	Sequence 73083, A
308	414	17.1	440	16	US-10-437-963-128633	Sequence 128633, A	381	325	13.4	414	15	US-10-425-114-59413	Sequence 59413, A
309	407.5	16.8	312	16	US-10-425-115-313908	Sequence 313308, A	382	325	13.4	416	15	US-10-425-114-59056	Sequence 59056, A
310	407	16.8	316	17	US-10-732-923-19289	Sequence 19289, A	383	325	13.4	416	15	US-10-425-114-65981	Sequence 65981, A
311	404.5	16.7	406	16	US-10-425-115-245402	Sequence 245402, A	384	325	13.4	417	15	US-10-425-114-59051	Sequence 59051, A
312	404.5	16.7	431	16	US-10-425-114-67044	Sequence 67044, A	385	325	13.4	418	15	US-10-425-114-67753	Sequence 67753, A
313	401.5	16.6	333	16	US-10-425-115-272995	Sequence 272995, A	386	325	13.4	419	15	US-10-425-114-66375	Sequence 66375, A
314	401.5	16.6	425	15	US-10-425-114-53960	Sequence 53960, A	387	325	13.4	419	15	US-10-425-114-66389	Sequence 66389, A
315	400.5	16.5	423	16	US-10-437-963-146611	Sequence 146611, A	388	325	13.4	419	15	US-10-425-114-67264	Sequence 67264, A
316	398.5	16.4	444	15	US-10-425-114-52078	Sequence 52078, A	389	325	13.4	420	15	US-10-425-114-66146	Sequence 66146, A
317	397.5	16.4	420	16	US-10-425-115-197935	Sequence 197935, A	390	325	13.4	420	15	US-10-425-114-73079	Sequence 73079, A
318	397.5	16.4	444	15	US-10-425-114-63026	Sequence 63026, A	391	325	13.4	422	15	US-10-425-114-66110	Sequence 66110, A
319	397.5	16.4	444	15	US-10-425-114-63935	Sequence 63935, A	392	325	13.4	422	15	US-10-425-114-66178	Sequence 66178, A
320	394	16.3	391	15	US-10-424-599-285116	Sequence 285116, A	393	325	13.4	422	15	US-10-425-114-66994	Sequence 66994, A
321	393.5	16.2	321	16	US-10-437-963-155839	Sequence 155839, A	394	325	13.4	422	15	US-10-425-114-72483	Sequence 72483, A
322	393	16.2	304	15	US-10-425-114-43121	Sequence 43121, A	395	325	13.4	423	15	US-10-425-114-66180	Sequence 66180, A
323	389.5	16.1	345	15	US-10-425-114-49653	Sequence 49653, A	396	325	13.4	425	15	US-10-425-114-66110	Sequence 66110, A
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325	388	16.0	419	16	US-10-425-115-273017	Sequence 273017, A	398	324	13.4	229	17	US-10-874-706-22	Sequence 22, Appl
326	386.5	16.0	308	15	US-10-369-493-3529	Sequence 3529, Ap	399	324	13.4	387	16	US-10-425-115-311502	Sequence 311502, A
327	385.5	15.9	414	16	US-10-437-963-150460	Sequence 150460, A	400	324	13.4	409	15	US-10-425-114-67522	Sequence 67522, A
328	383.5	15.8	294	15	US-10-369-493-5153	Sequence 5153, Ap	401	324	13.4	421	15	US-10-425-114-66461	Sequence 66461, A
329	383.5	15.8	392	20	US-11-021-464-21	Sequence 21, Appl	402	323.5	13.4	305	17	US-10-732-923-19267	Sequence 19267, A
330	382	15.8	347	17	US-10-732-923-19233	Sequence 19233, A	403	323.5	13.4	442	15	US-10-425-114-66181	Sequence 66181, A
331	379.5	15.7	400	15	US-10-424-599-14597	Sequence 144597, A	404	323	13.3	308	14	US-10-128-714-3338	Sequence 8338, Ap
332	378	15.6	317	15	US-10-425-114-50147	Sequence 50147, A	405	323	13.3	308	14	US-10-128-714-8338	Sequence 8338, Ap
333	378	15.6	342	17	US-10-732-923-19231	Sequence 19231, A	406	323	13.3	386	9	US-09-734-569-170	Sequence 170, App
334	367.5	15.2	338	15	US-10-424-599-221234	Sequence 221234, A	407	322.5	13.3	415	15	US-10-425-115-51062	Sequence 51062, A
335	365	15.1	382	15	US-10-424-599-275634	Sequence 275634, A	408	322	13.3	340	16	US-10-425-115-334170	Sequence 334170, A
336	363.5	15.0	364	17	US-10-732-923-19229	Sequence 19229, A	409	322	13.3	309	15	US-10-369-499-1876	Sequence 1876, Ap
337	361	14.9	339	17	US-10-732-923-19223	Sequence 19223, A	410	322	13.3	420	15	US-10-425-114-66118	Sequence 66118, A
338	360.5	14.9	327	15	US-10-425-114-64610	Sequence 64610, A	411	322	13.3	420	15	US-10-425-114-67195	Sequence 67195, A
339	359	14.8	334	16	US-10-425-114-64780	Sequence 64780, A	412	321.5	13.3	480	16	US-10-739-930-8166	Sequence 8166, Ap
340	357	14.7	335	16	US-10-425-115-204235	Sequence 204235, A	413	321	13.3	418	15	US-10-425-114-66173	Sequence 66173, A
341	356.5	14.7	335	16	US-10-425-115-195173	Sequence 195173, A	414	320	13.2	206	15	US-10-424-599-221239	Sequence 221239, A
342	354	14.6	326	15	US-10-369-493-2182	Sequence 2182, A	415	319	13.2	478	16	US-10-437-963-161560	Sequence 161560, A
343	353.5	14.6	225	15	US-10-425-114-67262	Sequence 67262, A	416	318	13.1	387	16	US-10-767-701-46663	Sequence 46663, A
344	349	14.4	357	16	US-10-369-493-22820	Sequence 22820, A	417	318	13.1	397	16	US-10-425-115-311495	Sequence 311495, A
345	348.5	14.4	375	16	US-10-767-701-43678	Sequence 43678, A	418	318	13.1	412	15	US-10-425-114-66054	Sequence 66054, A
346	347.5	14.3	378	15	US-10-424-599-240836	Sequence 240836, A	419	318	13.1	418	15	US-10-425-114-67091	Sequence 67091, A
347	347.5	14.3	410	9	US-09-796-766-10	Sequence 10, Appl	420	316.5	13.1	301	14	US-10-032-588-7194	Sequence 7194, Ap
348	345.5	14.3	410	15	US-10-659-199-10	Sequence 19924, A	421	316	13.0	288	16	US-10-408-765A-1631	Sequence 1631, Ap
349	345.5	14.3	364	17	US-10-732-923-19234	Sequence 19234, A	422	316	13.0	420	15	US-10-425-114-66170	Sequence 66170, A
350	344.5	14.2	270	15	US-10-425-114-52289	Sequence 52289, A	423	315.5	13.0	223	18	US-10-485-986-18	Sequence 18, Appl
351	340.5	14.1	312	15	US-10-369-493-3290	Sequence 3290, Ap	424	315	13.0	228	9	US-09-809-889-33	Sequence 33, Appl
352	336.5	13.9	269	16	US-10-425-115-224708	Sequence 224708, A	425	314	13.0	228	9	US-09-811-094-33	Sequence 33, Appl
353	336	13.9	270	16	US-10-425-115-351741	Sequence 351741, A	426	314	13.0	228	9	US-09-810-644-33	Sequence 33, Appl
354	336	13.9	382	16	US-10-767-701-42759	Sequence 42759, A	427	314	13.0	228	9	US-09-185-904A-33	Sequence 33, Appl
355	336	13.9	305	17	US-10-732-923-19213	Sequence 19213, A	428	314	13.0	228	11	US-09-809-889-33	Sequence 33, Appl
356	334.5	13.8	328	15	US-10-424-599-201843	Sequence 201843, A	429	314	13.0	228	11	US-09-809-889-33	Sequence 33, Appl
357	334.5	13.8	442	15	US-10-424-599-225734	Sequence 225734, A	430	314	13.0	228	11	US-09-811-131-33	Sequence 33, Appl
358	334	13.8	410	16	US-10-437-963-189967	Sequence 189967, A	431	314	13.0	298	11	US-09-811-131-33	Sequence 33, Appl
359	333.5	13.8	385	16	US-10-437-963-122906	Sequence 122906, A	432	314	13.0	228	16	US-10-763-399-6	Sequence 6, Appl1
360	332.5	13.7	382	16	US-10-437-963-115780	Sequence 115780, A	433	314	13.0	228	18	US-10-684-423-49	Sequence 49, Appl
361	331	13.7	387	16	US-10-425-115-311497	Sequence 311497, A	434	314	13.0	326	15	US-10-369-493-6333	Sequence 6333, Ap
362	329	13.6	387	16	US-10-425-115-311497	Sequence 311497, A	435	314	13.0	367	15	US-10-424-599-19653	Sequence 149653, A
363	328	13.5	324	15	US-10-369-493-2374	Sequence 2374, Ap	436	313	12.9	319	16	US-10-425-115-224694	Sequence 224694, A
364	327.5	13.5	335	15	US-10-369-493-3635	Sequence 3635, Ap	437	313	12.9	338	16	US-09-800-528-15	Sequence 15, Appl
365	327	13.5	381	14	US-10-425-115-224691	Sequence 224691, A	438	313	12.9	360	17	US-10-838-287-15	Sequence 15, Appl
366	327	13.5	420	15	US-10-425-114-66174	Sequence 66174, A	439	313	12.9	370	15	US-10-732-923-19323	Sequence 19323, A
367	327	13.5	305	17	US-10-732-923-19268	Sequence 19268, A	440	313	12.9	370	15	US-10-425-114-72421	Sequence 72421, A
368	326.5	13.5	337	16	US-10-437-963-118448	Sequence 118448, A	441	312.5	12.8	307	15	US-10-369-493-1450	Sequence 1450, Ap
369	326.5	13.5	315	16	US-10-425-115-224700	Sequence 224700, A	442	311	12.8	395	16	US-10-408-765A-3398	Sequence 2398, Ap
370	326	13.5	387	16	US-10-425-115-311498	Sequence 311498, A	443	310.5	12.8	310	15	US-10-128-714-8052	Sequence 8052, Ap
371	326	13.5	422	15	US-10-425-114-66159	Sequence 66159, A	444	309	12.8	310	15	US-10-320-797-3092	Sequence 3092, Ap
372	325.5	13.4	251	16	US-10-425-115-313909	Sequence 313909, A	445	309	12.8	372	15	US-10-369-493-6885	Sequence 6885, Ap
373	325.5	13.4	317	17	US-10-732-923-19236	Sequence 19236, A	446	308.5	12.7	318	9	US-09-801-368-252	Sequence 168017, A
374	325	13.4	367	16	US-10-425-115-311501	Sequence 311501, A	447	308.5	12.7	318	15	US-10-369-493-1421	Sequence 252, App
375	325	13.4	405	15	US-10-425-114-66251	Sequence 66251, A	448	308.5	12.7	318	15	US-10-369-493-1421	Sequence 1421, Ap
376	325	13.4					449	308	12.7	298	15	US-10-403-571-184	Sequence 154, App

450	308	12.7	298	16	US-10-763-398-5	Sequence 5, Appl1	523	287	11.8	315	17	US-10-732-923-19287	Sequence 19287, A
451	308	12.7	371	15	US-10-424-599-168016	Sequence 168016, A	524	286.5	11.8	321	15	US-10-415-378-11	Sequence 11, Appl1
452	307.5	12.7	380	16	US-10-425-115-346498	Sequence 346498, A	525	286.5	11.8	366	14	US-10-425-114-63867	Sequence 63867, A
453	307	12.7	273	15	US-10-424-599-265334	Sequence 265334, A	526	286	11.8	325	15	US-10-270-861-1	Sequence 1, Appl1
454	307	12.7	315	16	US-10-408-7654-1730	Sequence 1730, Ap	527	286	11.8	335	10	US-09-984-276-118	Sequence 118, App
455	307	12.7	315	16	US-10-343-903-19	Sequence 19, Appl	528	286	11.8	335	10	US-09-984-276-118	Sequence 118, App
456	305.5	12.6	304	17	US-10-732-923-19332	Sequence 19332, A	529	285	11.8	322	14	US-10-270-861-11	Sequence 11, Appl
457	305	12.6	368	15	US-10-369-493-4217	Sequence 4217, Ap	530	285	11.8	325	14	US-10-270-861-13	Sequence 13, Appl
458	305	12.6	377	15	US-10-369-493-1482	Sequence 1482, Ap	531	285	11.8	329	17	US-10-928-999-174	Sequence 174, App
459	304.5	12.6	298	16	US-10-408-7658-1680	Sequence 1680, Ap	532	284.5	11.7	224	15	US-10-369-493-12358	Sequence 12358, A
460	304	12.5	297	9	US-09-811-094-51	Sequence 31, Appl	533	284.5	11.7	337	16	US-10-425-115-256580	Sequence 256580, A
461	304	12.5	297	9	US-09-810-644-31	Sequence 31, Appl	534	284	11.7	310	17	US-10-732-923-19284	Sequence 19284, A
462	304	12.5	297	9	US-09-185-904A-31	Sequence 31, Appl	535	283	11.7	335	15	US-10-262-511-152	Sequence 152, App
463	304	12.5	297	11	US-09-809-827-31	Sequence 31, Appl	536	282	11.6	339	14	US-10-032-588-7183	Sequence 7183, Ap
464	304	12.5	297	11	US-09-809-889-31	Sequence 31, Appl	537	280	11.6	322	15	US-10-369-493-23200	Sequence 22200, A
465	304	12.5	297	11	US-09-811-131-31	Sequence 31, Appl	538	280	11.6	366	15	US-10-369-493-12653	Sequence 12653, A
466	304	12.5	297	11	US-09-811-132-31	Sequence 31, Appl	539	279	11.5	334	15	US-10-432-737-52	Sequence 52, Appl
467	304	12.5	297	16	US-10-408-7658-374	Sequence 374, App	540	279	11.5	334	17	US-10-732-923-19334	Sequence 19334, A
468	304	12.5	297	16	US-10-763-398-4	Sequence 4, Appl	541	278	11.5	288	17	US-10-732-923-19329	Sequence 19329, A
469	304	12.5	297	18	US-10-684-232-47	Sequence 47, Appl	542	277.5	11.5	313	15	US-10-369-493-6072	Sequence 6072, Ap
470	304	12.5	297	20	US-11-019-855-46	Sequence 46, Appl	543	277.5	11.5	313	15	US-10-369-493-6103	Sequence 6103, Ap
471	304	12.5	366	15	US-10-369-493-13350	Sequence 13350, A	544	277.5	11.5	314	15	US-10-369-493-21975	Sequence 21975, A
472	303	12.5	317	15	US-10-424-599-186641	Sequence 186641, A	545	277.5	11.5	730	15	US-10-425-114-59048	Sequence 59048, A
473	303	12.5	339	17	US-10-732-923-19215	Sequence 19215, A	546	277	11.4	935	17	US-10-732-923-19249	Sequence 19249, A
474	302.5	12.5	330	9	US-09-840-787-12	Sequence 12, Appl	547	276.5	11.4	731	17	US-10-732-923-19204	Sequence 19204, A
475	302.5	12.5	330	10	US-09-923-921A-2	Sequence 2, Appl1	548	276	11.4	288	17	US-10-732-923-19330	Sequence 19330, A
476	302.5	12.5	320	13	US-10-087-192-1716	Sequence 1716, Ap	549	275	11.3	373	15	US-10-369-493-22116	Sequence 22116, A
477	302.5	12.5	320	14	US-10-116-255-21	Sequence 21, Appl	550	274	11.3	300	15	US-10-369-493-5088	Sequence 5088, Ap
478	302.5	12.5	330	15	US-10-170-385-93	Sequence 93, Appl	551	274	11.3	335	15	US-10-369-493-5088	Sequence 1721, Ap
479	302.5	12.5	339	9	US-09-860-670-144	Sequence 144, App	552	273.5	11.3	277	15	US-10-369-493-2414	Sequence 2414, Ap
480	302.5	12.5	339	9	US-09-860-670-146	Sequence 146, App	553	273.5	11.3	277	15	US-10-369-493-2422	Sequence 2422, Ap
481	302.5	12.5	339	15	US-10-327-646-144	Sequence 144, App	554	273.5	11.3	521	16	US-10-425-115-197467	Sequence 197467, A
482	302.5	12.5	339	15	US-10-327-646-146	Sequence 146, App	555	273.5	11.3	670	16	US-10-425-115-197467	Sequence 197467, A
483	302	12.5	298	9	US-09-811-094-52	Sequence 32, Appl	556	273	11.2	290	16	US-10-767-701-32943	Sequence 32943, A
484	302	12.5	298	9	US-09-810-644-32	Sequence 32, Appl	557	272	11.2	232	9	US-09-796-766-4	Sequence 4, Appl1
485	302	12.5	298	9	US-09-185-904A-32	Sequence 32, Appl	558	272	11.2	232	16	US-10-659-199-4	Sequence 4, Appl1
486	302	12.5	298	11	US-09-809-827-32	Sequence 32, Appl	559	272	11.2	382	16	US-10-437-963-186043	Sequence 186043, A
487	302	12.5	298	11	US-09-809-889-32	Sequence 32, Appl	560	271	11.2	304	17	US-10-732-923-19197	Sequence 19197, A
488	302	12.5	298	11	US-09-811-131-32	Sequence 32, Appl	561	270.5	11.2	300	15	US-10-369-493-5919	Sequence 5919, Ap
489	302	12.5	298	11	US-09-811-132-32	Sequence 32, Appl	562	270.5	11.2	678	16	US-10-408-765A-499	Sequence 499, App
490	302	12.5	298	18	US-10-684-232-48	Sequence 48, Appl	563	270.5	11.2	678	16	US-10-408-765A-499	Sequence 2057, Ap
491	302	12.5	299	17	US-10-732-923-19301	Sequence 19301, A	564	270.5	11.2	678	17	US-10-732-923-19357	Sequence 19357, A
492	302	12.5	330	16	US-10-739-930-7445	Sequence 7445, Ap	565	270.5	11.2	678	17	US-10-732-923-19358	Sequence 19358, A
493	301.5	12.4	296	15	US-10-424-599-164627	Sequence 164627, A	566	270.5	11.2	680	15	US-10-291-172-339	Sequence 339, App
494	301.5	12.4	311	14	US-10-116-255-24	Sequence 24, Appl	567	270.5	11.2	680	15	US-10-221-278-339	Sequence 339, App
495	301.5	12.4	316	15	US-10-432-737-12	Sequence 12, Appl	568	270.5	11.2	684	11	US-09-764-875-1197	Sequence 1197, A
496	301.5	12.4	677	14	US-10-259-165-192	Sequence 192, App	569	270.5	11.2	684	15	US-10-158-057-331	Sequence 331, App
497	300.5	12.4	315	17	US-10-732-923-19343	Sequence 19343, A	570	269	11.1	706	17	US-10-732-923-19300	Sequence 19300, A
498	299.5	12.4	289	9	US-09-800-528-10	Sequence 10, Appl	571	267.5	11.0	307	17	US-10-732-923-19339	Sequence 19339, A
499	299.5	12.4	289	16	US-10-838-287-10	Sequence 10, Appl	572	267	11.0	307	17	US-10-732-923-19339	Sequence 19339, A
500	299.5	12.4	289	16	US-10-732-923-19333	Sequence 19333, A	573	267	11.0	374	15	US-10-425-114-59098	Sequence 59098, A
501	299.5	12.4	315	15	US-10-432-737-10	Sequence 10, Appl	574	267	11.0	332	16	US-10-425-114-59098	Sequence 59098, A
502	299.5	12.4	316	15	US-10-432-737-14	Sequence 14, Appl	575	266.5	11.0	333	14	US-10-270-861-9	Sequence 9, Appl1
503	299.5	12.3	300	17	US-10-732-923-19304	Sequence 19304, A	576	266	11.0	205	15	US-10-424-599-221237	Sequence 221237, A
504	298.5	12.3	382	16	US-10-739-930-7078	Sequence 7078, Ap	577	266	11.0	313	14	US-10-128-714-3052	Sequence 3052, Ap
505	298	12.3	300	17	US-10-732-923-19303	Sequence 19303, A	578	264.5	10.9	307	15	US-10-369-493-3514	Sequence 3514, Ap
506	297	12.3	260	16	US-10-425-115-322452	Sequence 322452, A	579	263.5	10.9	300	15	US-10-424-599-224710	Sequence 224710, A
507	296.5	12.2	283	15	US-10-369-493-4013	Sequence 4013, Ap	580	263	10.9	304	15	US-10-369-493-22277	Sequence 22277, A
508	295.5	12.2	283	15	US-10-732-923-19342	Sequence 19342, A	581	263	10.9	336	15	US-10-732-923-19315	Sequence 19315, A
509	295	12.2	310	14	US-10-043-487-352	Sequence 352, App	582	262	10.8	336	15	US-10-369-493-12689	Sequence 12689, A
510	293.5	12.1	229	15	US-10-424-599-219352	Sequence 219352, A	583	261.5	10.8	675	16	US-10-408-765A-852	Sequence 852, App
511	292.5	12.1	306	15	US-10-369-493-6116	Sequence 6116, Ap	584	261.5	10.8	675	17	US-10-732-923-19360	Sequence 19360, A
512	292.5	12.1	315	16	US-10-369-493-9062	Sequence 9062, Ap	585	261	10.8	333	15	US-10-369-493-6430	Sequence 6430, Ap
513	292.5	12.1	318	17	US-10-732-923-19290	Sequence 19290, A	586	261	10.8	674	9	US-09-941-340-2	Sequence 2, Appl1
514	291.5	12.1	328	16	US-10-739-930-10361	Sequence 10361, A	587	261	10.8	337	17	US-10-732-923-19186	Sequence 19186, A
515	291.5	12.0	295	16	US-10-67-701-43570	Sequence 43570, A	588	260	10.7	675	17	US-10-732-923-19285	Sequence 19285, A
516	290.5	12.0	349	15	US-10-320-797-3160	Sequence 3160, Ap	589	259.5	10.7	674	17	US-10-732-923-19341	Sequence 19341, A
517	289.5	11.9	300	17	US-10-732-923-19331	Sequence 19331, A	590	259.5	10.7	311	17	US-10-732-923-19374	Sequence 19374, A
518	289	11.9	304	15	US-10-432-737-8	Sequence 8, Appl1	591	259	10.7	101	16	US-10-425-115-229317	Sequence 229317, A
519	289	11.9	304	15	US-10-732-923-19322	Sequence 19322, A	592	259	10.7	308	17	US-10-732-923-19373	Sequence 19373, A
520	289	11.9	304	17	US-10-270-861-7	Sequence 7, Appl1	593	259	10.7	311	15	US-10-369-493-22088	Sequence 22088, A
521	288.5	11.9	390	16	US-10-425-115-311503	Sequence 311503, A	594	259	10.7	633	17	US-10-732-923-19317	Sequence 19317, A
522	287	11.8	261	16	US-10-425-115-348363	Sequence 348363, A	595	259	10.7	676	17	US-10-732-923-19359	Sequence 19359, A

596	259	10.7	682	17	US-10-732-923-19318	Sequence 19318, A	669	237.5	9.8	290	16	US-10-437-963-112774	Sequence 172774,
597	259	10.7	695	17	US-10-732-923-19316	Sequence 19316, A	670	237.5	9.8	351	14	US-09-840-787-19	Sequence 19, Appl
598	258.5	10.7	696	16	US-10-437-963-123597	Sequence 123597, A	671	237.5	9.8	331	19	US-10-116-255-20	Sequence 20, Appl
599	258.5	10.7	296	17	US-10-732-923-19338	Sequence 19338, A	672	236.5	9.8	290	15	US-10-262-511-146	Sequence 146, Appl
600	258.5	10.7	296	17	US-10-732-923-19350	Sequence 19350, A	673	236.5	9.8	303	17	US-10-732-923-19302	Sequence 19302, A
601	258.5	10.7	304	17	US-10-732-923-19202	Sequence 19202, A	674	236.5	9.8	322	16	US-10-437-963-170716	Sequence 170716, A
602	258.5	10.7	675	17	US-10-732-923-19361	Sequence 19361, A	675	236.5	9.8	332	17	US-10-732-923-19239	Sequence 19239, A
603	258.5	10.7	676	17	US-10-732-923-19385	Sequence 19385, A	676	236.5	9.8	322	17	US-10-732-923-19252	Sequence 19252, A
604	258	10.6	300	15	US-10-369-493-7009	Sequence 7009, Ap	677	236.5	9.8	404	17	US-10-732-923-19263	Sequence 19263, A
605	258	10.6	307	15	US-10-732-923-19291	Sequence 19291, Ap	678	236.5	9.8	409	16	US-10-408-765A-1089	Sequence 2089, Ap
606	257.5	10.6	676	17	US-10-732-923-19187	Sequence 19187, A	679	236.5	9.8	422	15	US-10-369-499-13366	Sequence 13366, A
607	256.5	10.6	291	15	US-10-108-260A-2476	Sequence 2476, Ap	680	236.5	9.8	620	16	US-10-437-963-160528	Sequence 160528, A
608	255.5	10.5	267	18	US-10-485-986-15	Sequence 15, Appl	681	236	9.7	56	9	US-09-864-761-45744	Sequence 45744, A
609	255.5	10.5	294	17	US-10-732-923-19218	Sequence 19218, A	682	236	9.7	245	16	US-10-425-115-311494	Sequence 311494, A
610	255	10.5	268	16	US-10-425-115-365390	Sequence 365390, A	683	236	9.7	300	14	US-10-270-861-35	Sequence 35, Appl
611	255	10.5	321	15	US-10-264-237-2737	Sequence 2737, Ap	684	236	9.7	300	17	US-10-732-923-19364	Sequence 19364, A
612	254	10.5	314	16	US-10-408-765A-2077	Sequence 2077, Ap	685	236	9.7	301	17	US-10-732-923-19175	Sequence 19175, A
613	254	10.5	368	16	US-10-723-860-2113	Sequence 2113, Ap	686	236	9.7	302	17	US-10-732-923-19264	Sequence 19264, A
614	254	10.5	418	17	US-10-732-923-19201	Sequence 19201, A	687	236	9.7	306	17	US-10-732-923-19174	Sequence 19174, A
615	253.5	10.5	157	15	US-10-424-599-277329	Sequence 277329, A	688	236	9.7	312	9	US-09-734-134-2	Sequence 2, Appl
616	253.5	10.5	157	15	US-10-424-599-268154	Sequence 268154, A	689	236	9.7	312	9	US-09-826-507-2	Sequence 2, Appl
617	253.5	10.5	364	16	US-10-843-132-2	Sequence 2, Appl	690	236	9.7	312	9	US-09-808-457-2	Sequence 2, Appl
618	253	10.4	240	16	US-10-425-115-224698	Sequence 224698	691	236	9.7	312	15	US-10-671-628-9	Sequence 9, Appl
619	253	10.4	256	16	US-10-104-047-2400	Sequence 2400, Ap	692	236	9.7	312	16	US-10-627-766-4	Sequence 4, Appl
620	253	10.4	320	16	US-10-739-930-6246	Sequence 6246, Ap	693	236	9.7	312	17	US-10-732-923-19365	Sequence 19365, A
621	252	10.4	228	15	US-10-264-049-4337	Sequence 4337, Ap	694	236	9.7	311	15	US-10-336-472-130	Sequence 130, Ap
622	251.5	10.4	177	16	US-10-767-701-47449	Sequence 47449, A	695	236	9.7	335	15	US-10-369-493-2203	Sequence 2203, Ap
623	251	10.4	314	15	US-10-369-493-22146	Sequence 22146, A	696	236	9.7	424	17	US-10-732-923-19228	Sequence 19228, A
624	250.5	10.3	340	16	US-10-437-963-182118	Sequence 182118, A	697	235.5	9.7	159	16	US-10-425-115-229319	Sequence 229319, A
625	249.5	10.3	595	17	US-10-732-923-19251	Sequence 19251, A	698	235	9.7	203	15	US-10-424-599-242604	Sequence 242604, A
626	248.5	10.3	368	17	US-10-732-923-19230	Sequence 19230, A	699	235	9.7	309	16	US-10-333-242A-4	Sequence 4, Appl
627	248	10.2	309	17	US-10-732-923-19372	Sequence 19372, A	700	234.5	9.7	161	14	US-10-083-357-768	Sequence 768, Ap
628	247.5	10.2	280	16	US-10-425-115-327948	Sequence 327948, A	701	234.5	9.7	312	15	US-10-369-493-5578	Sequence 5578, Ap
629	247.5	10.2	296	16	US-10-732-923-19258	Sequence 19258, A	702	234.5	9.7	334	15	US-10-424-599-241597	Sequence 241597, A
630	247.5	10.2	300	17	US-10-732-923-19225	Sequence 19225, A	703	234.5	9.7	366	16	US-10-425-115-216570	Sequence 216570, A
631	247.5	10.2	307	17	US-10-732-923-19337	Sequence 19337, A	704	234.5	9.7	409	17	US-10-732-923-19184	Sequence 19184, A
632	247	10.2	213	15	US-10-424-599-161854	Sequence 161854, A	705	234	9.7	447	9	US-09-941-340-4	Sequence 4, Appl
633	247	10.2	309	17	US-10-732-923-19170	Sequence 19170, A	706	233.5	9.6	270	15	US-10-262-511-148	Sequence 148, Ap
634	246.5	10.2	292	16	US-10-732-923-19170	Sequence 19170, A	707	233.5	9.6	286	15	US-10-262-511-144	Sequence 144, Ap
635	246.5	10.2	311	17	US-10-732-923-19371	Sequence 19371, A	708	233.5	9.6	289	15	US-10-108-260A-2530	Sequence 2530, Ap
636	246	10.1	258	15	US-10-424-599-272277	Sequence 272277, A	709	233.5	9.6	323	14	US-10-116-255-23	Sequence 23, Appl
637	245.5	10.1	289	14	US-10-116-255-25	Sequence 25, Appl	710	233.5	9.6	343	17	US-10-732-923-19209	Sequence 19209, A
638	245.5	10.1	289	17	US-10-874-706-33	Sequence 33, Appl	711	233.5	9.6	339	9	US-09-888-358-3	Sequence 3, Appl
639	245.5	10.1	300	17	US-10-732-923-19217	Sequence 19217, A	712	232.5	9.6	339	17	US-10-732-923-19262	Sequence 19262, A
640	245	10.1	281	15	US-10-424-599-272274	Sequence 272274, A	713	232	9.6	339	15	US-10-369-493-22571	Sequence 22571, A
641	245	10.1	309	9	US-09-884-814-8	Sequence 8, Appl	714	231	9.5	198	15	US-10-424-599-192882	Sequence 192882, A
642	245	10.1	309	13	US-10-001-051B-2	Sequence 2, Appl	715	231	9.5	296	15	US-10-369-493-5481	Sequence 5481, Ap
643	245	10.1	309	15	US-10-197-019-3	Sequence 3, Appl	716	231	9.5	286	17	US-10-732-923-19299	Sequence 19299, A
644	245	10.1	309	17	US-10-732-923-19366	Sequence 19366, A	717	230.5	9.5	358	15	US-10-369-493-1936	Sequence 12936, A
645	244.5	10.1	262	16	US-10-408-765A-12	Sequence 12, Appl	718	230	9.5	301	14	US-10-205-194-27	Sequence 27, Appl
646	244.5	10.1	311	17	US-10-732-923-19367	Sequence 19367, A	719	230	9.5	301	17	US-10-732-923-19389	Sequence 19389, A
647	244.5	10.1	727	15	US-10-424-599-246231	Sequence 246231, A	720	229.5	9.5	311	17	US-10-732-923-19319	Sequence 19319, A
648	243	10.0	56	9	US-09-864-761-45841	Sequence 45841, A	721	229.5	9.5	311	17	US-10-732-923-19320	Sequence 19320, A
649	242	10.0	309	9	US-09-884-814-1	Sequence 1, Appl	722	229.5	9.5	311	17	US-10-507-617-58	Sequence 58, Appl
650	242	10.0	309	14	US-10-874-814-6	Sequence 6, Appl	723	229.5	9.5	324	15	US-10-424-599-151145	Sequence 151145, A
651	242	10.0	309	14	US-10-270-861-34	Sequence 34, Appl	724	229.5	9.5	364	15	US-10-424-599-19125	Sequence 19125, A
652	242	10.0	309	14	US-10-265-689-1	Sequence 1, Appl	725	229	9.5	306	17	US-10-732-923-19309	Sequence 19309, A
653	242	10.0	309	15	US-10-336-472-132	Sequence 132, Appl	726	229	9.5	307	17	US-10-732-923-19309	Sequence 19309, A
654	242	10.0	309	15	US-10-671-628-8	Sequence 8, Appl	727	229	9.5	313	16	US-10-369-493-22398	Sequence 22398, A
655	242	10.0	309	17	US-10-802-440-8	Sequence 8, Appl	728	228.5	9.4	109	11	US-10-425-115-311500	Sequence 311500, A
656	242	10.0	309	17	US-10-616-865-8	Sequence 8, Appl	729	228.5	9.4	128	11	US-09-864-408A-5942	Sequence 6942, Ap
657	242	10.0	309	17	US-10-732-923-19368	Sequence 19368, A	730	228.5	9.4	296	16	US-10-732-923-19328	Sequence 19328, A
658	242	10.0	309	20	US-11-027-053-8	Sequence 8, Appl	731	228.5	9.4	361	16	US-10-425-115-321169	Sequence 321169, A
659	242	10.0	314	10	US-09-823-886A-4	Sequence 4, Appl	732	227.5	9.4	287	16	US-10-437-963-167292	Sequence 167292, A
660	242	10.0	333	15	US-10-369-493-5321	Sequence 5321, Ap	733	227.5	9.4	294	17	US-10-507-617-55	Sequence 5, Appl
661	242	10.0	400	17	US-10-732-923-19346	Sequence 19346, A	734	227.5	9.4	299	15	US-10-161-927-6	Sequence 6, Appl
662	241.5	10.0	426	17	US-10-732-923-19207	Sequence 19207, A	735	227	9.4	290	15	US-10-424-599-261701	Sequence 261701, A
663	240.5	9.9	310	17	US-10-732-923-19335	Sequence 19335, A	736	227	9.4	328	15	US-10-369-493-5588	Sequence 5688, Ap
664	239	9.9	312	17	US-10-732-923-19363	Sequence 19363, A	737	226	9.3	333	16	US-10-437-963-187039	Sequence 187039, A
665	239	9.9	372	17	US-10-732-923-19188	Sequence 19188, A	738	226	9.3	162	16	US-10-767-701-39705	Sequence 39705, A
666	238.5	9.8	204	6	US-10-767-701-42252	Sequence 42252, A	739	226	9.3	340	15	US-10-369-493-6168	Sequence 6168, Ap
667	238.5	9.8	351	9	US-09-868-358-4	Sequence 4, Appl	740	226	9.3	340	15	US-10-369-493-6169	Sequence 6169, Ap
668	238	9.8	306	17	US-10-732-923-19173	Sequence 19173, A	741	225.5	9.3	307	10	US-09-823-886A-2	Sequence 2, Appl

742	225.5	9.3	307	15	US-10-037-417-87	Sequence 87, Appl	1027	213.5	8.8	307	15	US-10-037-417-91	Sequence 91, Appl
743	225.5	9.3	307	17	US-10-802-440-6	Sequence 6, Appl1	1028	213.5	8.8	307	17	US-10-732-923-19169	Sequence 19169, A
744	225.5	9.3	307	17	US-10-616-865-6	Sequence 6, Appl1	1029	213	8.8	187	17	US-10-425-115-302749	Sequence 302749, A
745	225.5	9.3	307	20	US-11-027-053-6	Sequence 6, Appl1	1030	213	8.8	297	17	US-10-507-617-56	Sequence 56, Appl
746	225	9.3	180	9	US-09-796-766-8	Sequence 8, Appl1	1031	213	8.8	314	16	US-10-408-765A-498	Sequence 498, App
747	225	9.3	180	16	US-10-659-199-8	Sequence 8, Appl1	1032	213	8.8	314	16	US-10-408-765A-2204	Sequence 2204, App
748	225	9.3	756	16	US-10-437-963-194126	Sequence 194126, A	1033	213	8.8	314	16	US-10-408-765A-3015	Sequence 3015, Ap
749	224.5	9.3	274	17	US-10-732-923-193175	Sequence 193175, A	1034	213	8.8	314	17	US-10-507-617-13	Sequence 13, Appl
750	224.5	9.3	296	16	US-10-333-243A-2	Sequence 2, Appl1	1035	212.5	8.8	319	17	US-10-732-923-19324	Sequence 19324, A
751	224.5	9.3	296	16	US-10-732-923-19219	Sequence 19219, A	1036	212	8.7	59	9	US-09-864-761-44584	Sequence 44584, A
752	223.5	9.2	310	16	US-10-425-115-298610	Sequence 298610, A	1037	212	8.7	111	16	US-10-767-701-62427	Sequence 62427, A
753	223.5	9.2	379	16	US-10-491-733-26	Sequence 26, Appl	1038	212	8.7	299	17	US-10-732-923-19311	Sequence 19311, A
754	222.5	9.2	301	14	US-10-116-255-22	Sequence 22, Appl	1039	212	8.7	301	17	US-10-732-923-19326	Sequence 19326, A
755	222.5	9.2	301	15	US-10-297-022-4	Sequence 4, Appl1	1040	212	8.7	306	15	US-10-037-417-90	Sequence 90, Appl
756	222.5	9.2	301	17	US-10-732-923-19349	Sequence 19349, A	1041	212	8.7	366	15	US-10-369-493-22003	Sequence 22003, A
757	222.5	9.2	379	15	US-10-369-493-22753	Sequence 22753, A	1042	211.5	8.7	366	15	US-10-425-115-296314	Sequence 296314, A
758	222.5	9.2	379	15	US-10-369-493-22754	Sequence 22754, A	1043	211.5	8.7	116	15	US-10-369-493-13321	Sequence 13321, A
759	222	9.2	299	17	US-10-732-923-19171	Sequence 19171, A	1044	211.5	8.7	300	15	US-10-424-599-217619	Sequence 217619, A
760	222	9.2	301	17	US-10-732-923-19336	Sequence 19336, A	1045	211.5	8.7	301	17	US-10-732-923-19190	Sequence 19190, A
761	222	9.2	319	17	US-10-732-923-19191	Sequence 19191, A	1046	211.5	8.7	369	16	US-10-437-963-146330	Sequence 146330, A
762	221.5	9.1	183	14	US-10-116-255-27	Sequence 27, Appl	1047	211	8.7	216	15	US-10-108-260A-3165	Sequence 3165, Ap
763	221.5	9.1	266	16	US-10-425-115-344306	Sequence 344306, A	1048	211	8.7	301	16	US-10-408-765A-541	Sequence 541, App
764	221.5	9.1	316	17	US-10-732-923-19237	Sequence 19237, A	1049	211	8.7	301	16	US-10-408-765A-19347	Sequence 19347, A
765	221.5	9.1	345	15	US-10-425-114-66317	Sequence 66317, A	1050	211	8.7	301	17	US-10-732-923-19348	Sequence 19348, A
766	221	9.1	186	15	US-10-437-963-237114	Sequence 237114, A	1051	210.5	8.7	300	14	US-10-116-255-35	Sequence 35, Appl
767	221	9.1	233	16	US-10-437-963-150461	Sequence 150461, A	1052	210	8.7	220	16	US-10-425-115-224690	Sequence 224690, A
768	221	9.1	301	15	US-10-369-493-4140	Sequence 4140, Ap	1053	210	8.7	307	17	US-10-732-923-19347	Sequence 19347, A
769	221	9.1	305	17	US-10-732-923-19312	Sequence 19312, A	1054	210	8.7	307	15	US-10-363-616-286	Sequence 286, App
770	221	9.1	317	16	US-10-437-963-134602	Sequence 134602, A	1055	210	8.7	409	14	US-10-369-493-3954	Sequence 3954, App
771	221	9.1	368	15	US-10-369-493-1895	Sequence 1895, Ap	1056	209.5	8.6	301	14	US-10-116-255-33	Sequence 33, Appl
772	221	9.1	459	17	US-10-732-923-19313	Sequence 19313, A	1057	209.5	8.6	301	17	US-10-732-923-19351	Sequence 19351, A
773	220.5	9.1	301	16	US-10-343-903-27	Sequence 27, Appl	1058	209.5	8.6	302	17	US-10-732-923-19260	Sequence 19260, A
774	220	9.1	267	15	US-10-424-599-241909	Sequence 241909, A	1059	209	8.6	115	16	US-10-767-701-42307	Sequence 42307, A
775	219.5	9.1	254	14	US-10-262-511-150	Sequence 150, App	1060	209	8.6	284	17	US-10-732-923-19288	Sequence 19288, A
776	219.5	9.1	307	14	US-10-270-861-33	Sequence 33, Appl	1061	209	8.6	306	17	US-10-732-923-19224	Sequence 19224, A
777	219.5	9.1	307	15	US-10-037-417-88	Sequence 88, Appl	1062	209	8.6	301	16	US-10-739-930-7595	Sequence 7595, Ap
778	219.5	9.1	307	15	US-10-671-628-7	Sequence 7, Appl1	1063	208.5	8.6	301	16	US-10-648-593-248	Sequence 248, App
779	219.5	9.1	311	15	US-10-369-493-22196	Sequence 22196, A	1064	208.5	8.6	301	17	US-10-732-923-19352	Sequence 19352, A
809	219.5	9.1	323	14	US-10-370-861-36	Sequence 36, Appl	1065	208.5	8.6	337	17	US-10-732-923-19261	Sequence 19261, A
873	219.5	9.1	323	14	US-10-063-742-126	Sequence 126, App	1066	208	8.6	314	17	US-10-732-923-19235	Sequence 19235, A
948	219.5	9.1	323	14	US-10-013-909A-406	Sequence 406, App	1067	207.5	8.6	304	14	US-10-116-255-26	Sequence 26, Appl
995	219.5	9.1	323	17	US-10-972-317-126	Sequence 126, App	1068	207.5	8.6	304	17	US-10-965-859-53	Sequence 53, Appl
996	219	9.0	169	16	US-10-739-920-9171	Sequence 9171, Ap	1069	207.5	8.6	317	15	US-10-424-599-276094	Sequence 276094, A
997	219	9.0	306	17	US-10-732-923-19310	Sequence 19310, A	1070	207.5	8.6	368	15	US-10-310-154-652	Sequence 652, App
998	219	9.0	356	13	US-10-108-605-269	Sequence 269, App	1071	207.5	8.6	358	17	US-10-732-923-492	Sequence 492, App
999	219	9.0	364	15	US-10-424-599-168159	Sequence 168159, A	1072	207	8.5	299	15	US-10-369-493-6084	Sequence 6084, Ap
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1001	218.5	9.0	358	15	US-10-369-493-4106	Sequence 4106, Ap	1074	207	8.5	274	10	US-09-876-997-244	Sequence 244, App
1002	218	9.0	320	16	US-10-425-115-302750	Sequence 302750, A	1075	207	8.5	274	17	US-10-643-835-244	Sequence 244, App
1003	218	9.0	306	17	US-10-732-923-19222	Sequence 19222, A	1076	207	8.5	307	15	US-10-369-493-3697	Sequence 3697, App
1004	218	9.0	309	15	US-10-369-493-6038	Sequence 6038, Ap	1077	206.5	8.5	219	16	US-10-437-963-158889	Sequence 158889, A
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1008	217	9.0	282	15	US-10-425-114-39195	Sequence 39195, A	1081	206.5	8.5	341	15	US-10-425-114-552234	Sequence 552234, A
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1018	215	8.9	327	16	US-10-437-963-125993	Sequence 125993, A	1091	205	8.5	359	9	US-10-507-617-57	Sequence 57, Appl
1019	215	8.9	362	16	US-10-425-115-192956	Sequence 192956, A	1092	205	8.5	314	17	US-09-925-301-1137	Sequence 1127, Ap
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1021	214.5	8.9	301	16	US-10-437-963-174122	Sequence 174122, A	1094	205	8.5	361	16	US-10-684-765A-475	Sequence 475, Appl
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1023	214.5	8.9	311	17	US-10-732-923-19221	Sequence 19221, A	1096	205	8.5	361	17	US-10-734-049A-356	Sequence 356, App
1024	214.5	8.9	340	17	US-10-732-923-19327	Sequence 19327, A	1097	205	8.5	394	15	US-10-264-049-2722	Sequence 2722, Ap
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1251	181.5	7.5	219	15	US-10-732-923-19226	Sequence 19226, A	1324	163	6.7	184	16	US-10-755-889-668	Sequence 668, App
1252	181.5	7.5	331	17	US-10-732-923-19282	Sequence 19282, A	1325	162.5	6.7	94	15	US-10-424-599-243465	Sequence 243465,
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1263	179	7.4	273	15	US-10-369-493-4052	Sequence 4052, Ap	1336	161.5	6.7	313	15	US-10-369-493-3110	Sequence 3110, Ap
1264	178.5	7.4	194	17	US-10-732-923-19370	Sequence 19370, A	1337	161.5	6.7	189	9	US-09-821-725-5	Sequence 5, Appl
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